

NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 412
; LENGTH: 1184
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-412

Query Match 54.7%; Score 35; DB 1; Length 1184;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKRYDREPLG 11
|||
Db 723 KKRDRTFLVG 732

RESULT 2
US-10-793-626-66
; Sequence 66, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-66

Query Match 51.6%; Score 33; DB 1; Length 297;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 KKRYDREFL--LGF 12
|||
Db 107 KKRYDEKYYHSLGF 120

RESULT 3
US-10-793-626-746
; Sequence 746, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 746
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-746

Query Match 51.6%; Score 33; DB 1; Length 297;
Best Local Similarity 50.0%; Pred. No. 14;

Matches 7; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
QY 1 KKRYDREFL--LGF 12
|||
Db 107 KKRYDEKYYHSLGF 120

RESULT 4
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Seache-Crain, Birgit
; APPLICANT: Andarmati, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1234
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

Query Match 50.0%; Score 32; DB 1; Length 169;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKRYDRE 7
|||
Db 55 KARYDRE 61

RESULT 5
US-10-821-234-915
; Sequence 915, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Seache-Crain, Birgit
; APPLICANT: Andarmati, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 915
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-915

Query Match 50.0%; Score 32; DB 1; Length 478;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKRYDREFL 9
|||
Db 384 REAYDRDRL 392

RESULT 6
US-11-074-176-98
; Sequence 98, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kleenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Pell, Andrea Accarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-98

Query Match 50.0%; Score 32; DB 7; Length 565;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KRYDREFLLG 11
| | | | |
Db 97 KDRHGRSLLG 107

RESULT 7
US-10-793-626-3112
; Sequence 3112, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3112
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3112

Query Match 48.4%; Score 31; DB 1; Length 311;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KRYDREFLLG 11
| | | | |
Db 118 KRRKQTFLLG 127

RESULT 8
US-10-793-626-3184
; Sequence 3184, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3184
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3184

Query Match 48.4%; Score 31; DB 1; Length 567;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 KRYDREFLLG 11
| | | | |
Db 97 KDRHGRSLLG 107

RESULT 9
US-10-981-873-41
; Sequence 41, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-873-41

Query Match 46.9%; Score 30; DB 1; Length 211;
Best Local Similarity 71.4%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 KRYDREF 8
| | | | |
Db 87 RRYDSEF 93

RESULT 10
US-10-793-626-3236
; Sequence 3236, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09

/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3236
/ LENGTH: 411
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-3236

Query Match 46.9%; Score 30; DB 1; Length 411;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRYDREFL 9
DB 234 KRYNRETL 241

RESULT 11
US-11-074-176-306
/ Sequence 306, Application US/11074176
/ Publication No. US20050250135A1
/ GENERAL INFORMATION:
/ APPLICANT: Klaenhammer, Todd R.
/ APPLICANT: Russell, William M.
/ APPLICANT: Altermann, Eric
/ APPLICANT: McAuliffe, Olivia
/ TITLE OF INVENTION: Nucleic Acid Sequences Encoding
/ TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
/ FILE REFERENCE: 5051-694
/ CURRENT APPLICATION NUMBER: US/11/074,176
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: 60/551,161
/ PRIOR FILING DATE: 2004-03-08
/ NUMBER OF SEQ ID NOS: 381
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 306
/ LENGTH: 718
/ TYPE: PRT
/ ORGANISM: Lactobacillus acidophilus
US-11-074-176-306

Query Match 46.9%; Score 30; DB 7; Length 718;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 RYDREFLG 11
DB 353 RFDKRVLVG 361

RESULT 12
US-11-074-176-18
/ Sequence 18, Application US/11074176
/ Publication No. US20050250135A1
/ GENERAL INFORMATION:
/ APPLICANT: Klaenhammer, Todd R.
/ APPLICANT: Russell, William M.
/ APPLICANT: Altermann, Eric
/ APPLICANT: McAuliffe, Olivia
/ APPLICANT: Perill, Andrea Azcarate
/ TITLE OF INVENTION: Nucleic Acid Sequences Encoding
/ TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
/ FILE REFERENCE: 5051-694
/ CURRENT APPLICATION NUMBER: US/11/074,176
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: 60/551,161
/ PRIOR FILING DATE: 2004-03-08
/ NUMBER OF SEQ ID NOS: 381
/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 18
/ LENGTH: 723
/ TYPE: PRT
/ ORGANISM: Lactobacillus acidophilus
US-11-074-176-18

Query Match 46.9%; Score 30; DB 7; Length 723;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 RYDREFLG 11
DB 358 RFDKRVLVG 366

RESULT 13
US-10-793-626-3324
/ Sequence 3324, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: P03480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3324
/ LENGTH: 944
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-3324

Query Match 46.9%; Score 30; DB 1; Length 944;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRYDREFL 9
DB 767 KRYNRETL 774

RESULT 14
US-11-057-058-62
/ Sequence 62, Application US/11057058
/ Publication No. US20050244400A1
/ GENERAL INFORMATION:
/ APPLICANT: Lebowitz, Jonathan
/ APPLICANT: Maga, John
/ TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
/ FILE REFERENCE: SYM-011
/ CURRENT APPLICATION NUMBER: US/11/057,058
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: US 60/543,812
/ PRIOR FILING DATE: 2004-02-10
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 62
/ LENGTH: 1827
/ TYPE: PRT
/ ORGANISM: Rabbit sp.
US-11-057-058-62

Query Match 46.9%; Score 30; DB 7; Length 1827;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DREFLG 11

Db 731 DREFLWG 737

```

RESULT 15
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_Gene Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916

```

```

Query Match 46.9%; Score 30; DB 1; Length 3002;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Oy 3 RYDREFLG 11
Db 2979 KYDKDYLSG 2987

Search completed: November 29, 2005, 23:04:37
Job time : 3.25 secs

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OM protein - protein search, using SW model

Run on: November 29, 2005, 22:52:34 ; Search time 93.5455 Seconds
(without alignments)
53.599 Million cell updates/sec

Title: US-10-019-198a-1
Perfect score: 64
Sequence: 1 KRYDRFLGFG 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main.*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.rep.*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.rep.*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.rep.*
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.rep.*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	16	3	US-09-973-473-9
2	64	100.0	16	3	US-09-973-473-11
3	53	82.8	16	3	US-09-973-473-10
4	53	82.8	1756	5	US-10-450-763-50799
5	44	68.8	226	4	US-10-335-977-9703
6	44	68.8	339	4	US-10-335-977-6269
7	44	68.8	553	4	US-10-335-977-6270
8	44	68.8	556	4	US-10-335-977-6271
9	42	62.5	732	4	US-10-437-963-114937
10	40	62.5	941	4	US-10-259-194A-312
11	40	62.5	950	4	US-10-425-115-28367
12	40	62.5	1516	4	US-10-437-963-187843
13	40	62.5	2479	4	US-10-334-143-69
14	40	62.5	2872	5	US-10-783-528-116
15	39	60.9	16	3	US-09-973-473-12
16	39	60.9	121	4	US-10-425-115-288687
17	39	60.9	142	4	US-10-424-599-154949
18	39	60.9	310	4	US-10-369-493-17304
19	39	60.9	543	5	US-10-501-282-4464
20	39	60.9	568	5	US-10-501-282-4466
21	39	60.9	571	5	US-10-501-282-4468
22	39	60.9	1415	4	US-10-437-963-169368
23	39	60.9	1666	6	US-11-097-143-42954
24	38	59.4	449	4	US-10-425-114-55721
25	38	59.4	449	4	US-10-425-115-357901
26	38	59.4	643	4	US-10-425-115-357898
27	37.5	58.6	1418	4	US-10-369-493-22315

28	37	57.8	76	4	US-10-767-701-51018	Sequence 51018, A
29	37	57.8	192	4	US-10-437-963-154057	Sequence 154057, A
30	37	57.8	211	4	US-10-425-115-328208	Sequence 328208, A
31	37	57.8	267	3	US-09-911-781-24	Sequence 24, Appl
32	37	57.8	267	3	US-09-976-800-106	Sequence 106, App
33	37	57.8	267	3	US-10-138-838-106	Sequence 106, App
34	37	57.8	267	4	US-10-139-031-106	Sequence 106, App
35	37	57.8	267	4	US-10-138-905-106	Sequence 106, App
36	37	57.8	267	4	US-10-138-916-106	Sequence 106, App
37	37	57.8	267	4	US-10-139-236-106	Sequence 106, App
38	37	57.8	267	4	US-10-139-218-106	Sequence 24, Appl
39	37	57.8	267	4	US-10-400-902-24	Sequence 106, App
40	37	57.8	267	4	US-10-405-660-106	Sequence 106, App
41	37	57.8	267	4	US-10-138-898-106	Sequence 106, App
42	37	57.8	381	4	US-10-767-701-36815	Sequence 36815, A
43	37	57.8	521	4	US-10-425-114-43422	Sequence 43422, A
44	37	57.8	570	4	US-10-282-122A-65941	Sequence 65941, A
45	37	57.8	670	3	US-09-833-245-1304	Sequence 1304, Ap

ALIGNMENTS

RESULT 1
US-09-973-473-9
; Sequence 9, Application US/09973473
; Publication No. US20030041341A1
; GENERAL INFORMATION:
; APPLICANT: TREMBLAY, Michel
; APPLICANT: SONENBERG, Nahum
; APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
; TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
; FILE REFERENCE: 514012000400
; CURRENT APPLICATION NUMBER: US/09/973,473
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/CA00/00388
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,559
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/179,743
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-473-9
Query Match 100.0%; Score 64; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRYDRFLGFG 12
DB 1 KRYDRFLGFG 12
RESULT 2
US-09-973-473-11
; Sequence 11, Application US/09973473
; Publication No. US20030041341A1
; GENERAL INFORMATION:
; APPLICANT: SONENBERG, Nahum
; APPLICANT: TREMBLAY, Michel
; APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
; TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
; FILE REFERENCE: 514012000400
; CURRENT APPLICATION NUMBER: US/09/973,473

CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 16
TYPE: PRT
ORGANISM: Danio rerio
US-09-973-473-11

Query Match 100.0%; Score 64; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KKYRDEFLGF 12
Db 1 KKYRDEFLGF 12

RESULT 3
US-09-973-473-10
Sequence 10, Application US/09973473
Publication No. US20030041341A1
GENERAL INFORMATION:
APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, Michel
APPLICANT: TSUKIYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-973-473-10

Query Match 82.8%; Score 53; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 0.01;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKYRDEFLGF 12
Db 1 KKYRDEFLGF 12

RESULT 4
US-10-450-763-50799
Sequence 50799, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50799
LENGTH: 1756
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (49)..(59)
OTHER INFORMATION: TYPE I ANTIFREEZE PROTEIN SIGNATURE domain identified by
OTHER INFORMATION: EMATRIX, accession number PR00308C, p-value=8.013e-09, raw score
OTHER INFORMATION: 3.83
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1689)..(1756)
OTHER INFORMATION: eIF4-gamma/eIF5/eIF2-epsilon domain identified by Pfam,
OTHER INFORMATION: accession name IF5_eIF4_eIF2, E-value=0.0038, Pfam score of 4.4
NAME/KEY: misc_feature
LOCATION: (1)..(1756)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-50799

Query Match 82.8%; Score 53; DB 5; Length 1756;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKYRDEFLGF 12
Db 790 KKYRDEFLGF 801

RESULT 5
US-10-335-977-9703
Sequence 9703, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNTX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9703:
SEQUENCE CHARACTERISTICS:

LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...226
SEQUENCE DESCRIPTION: SEQ ID NO: 9703:
US-10-335-977-9703

Query Match 68.8%; Score 44; DB 4; Length 226;
Best Local Similarity 55.6%; Pred. No. 7.3;
Matches 10; Conservative 2; Mismatches 0; Indels 6; Gaps 1;
QY 1 KRYDREF-----LLGF 12
|||:||||
Db 129 KRYEKEFNLLMWGLGF 146

RESULT 6
US-10-335-977-6269
; Sequence 6269, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...339
; SEQUENCE DESCRIPTION: SEQ ID NO: 6269:
US-10-335-977-6269

Query Match 68.8%; Score 44; DB 4; Length 339;

Best Local Similarity 55.6%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 0; Indels 6; Gaps 1;
QY 1 KRYDREF-----LLGF 12
|||:||||
Db 210 KRYEKEFNLLMWGLGF 227

RESULT 7
US-10-335-977-6270
; Sequence 6270, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...553
; SEQUENCE DESCRIPTION: SEQ ID NO: 6270:
US-10-335-977-6270

Query Match 68.8%; Score 44; DB 4; Length 553;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 0; Indels 6; Gaps 1;
QY 1 KRYDREF-----LLGF 12
|||:||||
Db 369 KRYEKEFNLLMWGLGF 386

RESULT 8
US-10-335-977-6271
; Sequence 6271, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTV-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6271:
SEQUENCE CHARACTERISTICS:
LENGTH: 556 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...556
SEQUENCE DESCRIPTION: SEQ ID NO: 6271:
US-10-335-977-6271
Query Match 68.8%; Score 44; DB 4; Length 556;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 0; Indels 6; Gaps 1;
QY 1 KRRYDRER-----LLGF 12
Db 372 KRRYKEKERNLWVGLGF 389
RESULT 9
US-10-437-963-114937
Sequence 114937, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Mu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114937

LENGTH: 732
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_18580C.1.pep
US-10-437-963-114937
Query Match 65.6%; Score 42; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DREPLRGF 12
Db 186 DREPLRGF 193
RESULT 10
US-10-259-194A-312
Sequence 312, Application US/10259194A
Publication No. US20040010815A1
GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemlan, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Rickert, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 312
LENGTH: 941
TYPE: PRT
ORGANISM: Oryza sativa
US-10-259-194A-312
Query Match 62.5%; Score 40; DB 4; Length 941;
Best Local Similarity 77.8%; Pred. No. 1,7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRRYDRERFL 10
Db 226 KRRYDRERFLV 234
RESULT 11
US-10-425-115-282367
Sequence 282367, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115

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/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 282367
/ LENGTH: 950
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_20617C.1.pep
US-10-425-115-282367
```

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Query Match          62.5%; Score 40; DB 4; Length 950;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

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Qy      1 KRYDREFLLG 11
        ||| ||| :|
Db      753 KKRTRDFQVG 763
```

```
RESULT 12
US-10-437-963-187843
/ Sequence 187843, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Bardazuk, Brad
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5322)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 187843
/ LENGTH: 1516
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(1516)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_84506C.1.pep
US-10-437-963-187843
```

```
Query Match          62.5%; Score 40; DB 4; Length 1516;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KRYDREFLL 10
        ||| ||| :|
Db      552 RKRYSRDFLL 561
```

```
RESULT 13
US-10-334-143-69
/ Sequence 69, Application US/10334143
/ Publication No. US20040009549A1
/ GENERAL INFORMATION:
/ APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
/ APPLICANT: SUDARSANAM, SUCHA
/ TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
/ FILE REFERENCE: 038602/1543
/ CURRENT APPLICATION NUMBER: US/10/334,143
/ CURRENT FILING DATE: 2002-12-31
/ PRIOR APPLICATION NUMBER: 60/343,169
/ PRIOR FILING DATE: 2001-12-31
```

```
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 69
/ LENGTH: 2479
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (2479)
/ OTHER INFORMATION: Variable amino acid
US-10-334-143-69
```

```
Query Match          62.5%; Score 40; DB 4; Length 2479;
Best Local Similarity 63.6%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      2 KRYDREFLLGF 12
        ||| ||| :|
Db      2360 KRYDPELILGY 2370
```

```
RESULT 14
US-10-783-528-116
/ Sequence 116, Application US/10783528
/ Publication No. US20040219579A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natsaha
/ APPLICANT: Gish, Kurt
/ APPLICANT: Wilson, Keith
/ APPLICANT: Zlotnik, Albert
/ TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
/ FILE REFERENCE: 05882, 0191.NPUS01
/ CURRENT APPLICATION NUMBER: US/10/783,528
/ CURRENT FILING DATE: 2004-02-19
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 116
/ LENGTH: 2872
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-783-528-116
```

```
Query Match          62.5%; Score 40; DB 5; Length 2872;
Best Local Similarity 63.6%; Pred. No. 5.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 KRYDREFLLGF 12
        ||| ||| :|
Db      2049 KRYDPELILGY 2059
```

```
RESULT 15
US-09-973-473-12
/ Sequence 12, Application US/09973473
/ Publication No. US20030041341A1
/ GENERAL INFORMATION:
/ APPLICANT: SONENBERG, Nahum
/ APPLICANT: TREMBLAY, Michel
/ APPLICANT: TSUKIYAMA-KOHARA, KYOKO
/ TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
/ TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
/ FILE REFERENCE: 514012000400
/ CURRENT APPLICATION NUMBER: US/09/973,473
/ CURRENT FILING DATE: 2001-10-03
/ PRIOR APPLICATION NUMBER: PCT/CA00/00388
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: 60/128,559
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: 60/179,743
/ PRIOR FILING DATE: 2000-02-02
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 12
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-973-473-12

Query Match 60.9%; Score 39; DB 3; Length 16;
Best Local Similarity 80.0%; Pred. No. 4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKRYDREFLL 10
||:|||||
Db 1 KKQYDREQLL 10

Search completed: November 29, 2005, 23:10:26
Job time : 94.5455 secs

Thu Dec 1 11:53:09 2005

US-10-019-198A-1.rat

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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:45:04 ; Search time 28.6364 Seconds
(without alignments)
34.645 Million cell updates/sec

Title: US-10-019-198A-1
Perfect score: 64
Sequence: 1 KRYDRFLGF 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
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4: /cgn2_6/prodata/1/1aa/BCTUS COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	1560	US-09-264-512B-2	Sequence 2, Appl
2	53	82.8	977	US-09-949-016-8518	Sequence 8518, Ap
3	37	57.8	82	US-09-248-796A-27703	Sequence 27703, A
4	37	57.8	267	US-09-302-620B-106	Sequence 106, App
5	37	57.8	267	US-09-911-781-24	Sequence 24, Appl
6	37	57.8	267	US-10-400-902-24	Sequence 24, Appl
7	37	57.8	267	5204252-2	Patent No. 5204252
8	37	57.8	268	5204252-4	Patent No. 5204252
9	37	57.8	347	US-09-270-767-40048	Sequence 40048, A
10	37	57.8	347	US-09-270-767-55264	Sequence 55264, A
11	37	57.8	347	US-09-302-540-14261	Sequence 14261, A
12	37	57.8	599	US-08-954-333-7	Sequence 7, Appl
13	37	57.8	602	US-09-248-796A-19839	Sequence 19839, A
14	36	56.2	451	US-09-489-035A-8459	Sequence 8459, Ap
15	35	54.7	55	US-09-270-767-58606	Sequence 58606, A
16	35	54.7	317	US-08-555-722-8	Sequence 8, Appl
17	35	54.7	317	US-09-384-301-8	Sequence 8, Appl
18	35	54.7	317	US-09-949-016-10766	Sequence 10766, A
19	35	54.7	348	US-09-107-532A-6607	Sequence 6607, Ap
20	35	54.7	349	US-09-105-390-48	Sequence 48, Appl
21	35	54.7	377	US-09-105-390-64	Sequence 64, Appl
22	35	54.7	385	US-09-134-000C-4393	Sequence 4393, Ap
23	35	54.7	435	US-09-248-796A-18814	Sequence 18814, A
24	35	54.7	574	US-09-252-991A-29351	Sequence 29351, A
25	35	54.7	581	US-09-540-236-2739	Sequence 2739, Ap
26	35	54.7	803	US-08-907-166-4	Sequence 4, Appl
27	35	54.7	803	US-09-391-340-4	Sequence 4, Appl

ALIGNMENTS

28	35	54.7	1184	1	US-08-918-914-1	Sequence 1, Appl
29	35	54.7	1184	2	US-08-996-083-3	Sequence 3, Appl
30	35	54.7	1184	2	US-09-991-181-124	Sequence 124, App
31	35	54.7	1184	2	US-09-990-444-124	Sequence 124, App
32	35	54.7	1184	2	US-09-997-333-124	Sequence 124, App
33	35	54.7	1184	2	US-09-992-598-124	Sequence 43382, A
34	34	53.1	154	2	US-09-270-767-43382	Sequence 45396, A
35	34	53.1	189	2	US-09-270-767-45396	Sequence 110, App
36	34	53.1	189	2	US-09-265-585C-110	Sequence 3246, App
37	34	53.1	200	2	US-09-540-236-3246	Sequence 129, App
38	34	53.1	205	2	US-09-265-585C-129	Sequence 50, Appl
39	34	53.1	206	2	US-09-186-276B-50	Sequence 50, Appl
40	34	53.1	206	2	US-08-842-445-50	Sequence 50, Appl
41	34	53.1	206	2	US-09-186-188B-50	Sequence 50, Appl
42	34	53.1	206	2	US-09-265-585C-50	Sequence 50, Appl
43	34	53.1	263	1	US-08-088-633-4	Sequence 4, Appl
44	34	53.1	263	1	US-08-245-756-4	Sequence 4, Appl
45	34	53.1	263	1	US-08-441-750-4	Sequence 4, Appl

RESULT 1
US-09-264-512B-2
; Sequence 2, Application US/09264512B
; Patent No. 6610508
; GENERAL INFORMATION:
; APPLICANT: Henze, Matthias W.
; APPLICANT: De Gregorio, Bruno
; TITLE OF INVENTION: TRANSLATION DRIVER SYSTEM AND METHODS FOR USE THEREOF
; FILE REFERENCE: 9882-004
; CURRENT APPLICATION NUMBER: US/09/264,512B
; CURRENT FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-512B-2

Query Match 100.0%; Score 64; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRYDRFLGF 12
DB 569 KRYDRFLGF 580
RESULT 2
US-09-949-016-8518
; Sequence 8518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8518
; LENGTH: 977
; TYPE: PRT

ORGANISM: Human
US-09-949-016-8518

Query Match 82.8%; Score 53; DB 2; Length 977;
Best Local Similarity 83.3%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKRYDREFLLGF 12
|||:|||||
DB 13 KKQYDREFLLDF 24

RESULT 3

US-09-248-796A-27703
Sequence 27703, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Kelch Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248.796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074.725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096.409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 27703
LENGTH: 82
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (10)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-27703

Query Match 57.8%; Score 37; DB 2; Length 82;
Best Local Similarity 66.7%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKRYDREFLLGF 12
|||:|||||
DB 45 KKRTDREFKSNF 56

RESULT 4

US-09-302-620B-106
Sequence 106, Application US/09302620B
Patent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Esheo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleason, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
FILE REFERENCE: 1010-16.seg
CURRENT APPLICATION NUMBER: US/09/302.620B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 106
LENGTH: 267

TYPE: PRT
ORGANISM: Candida tropicalis
US-09-302-620B-106

Query Match 57.8%; Score 37; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DREFLLGF 12
|||:||||
DB 175 DREFVIGF 182

RESULT 5

US-09-911-781-24
Sequence 24, Application US/09911781
Patent No. 6673613
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Elrich, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAP (1010-49)
CURRENT APPLICATION NUMBER: US/09/911.781
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
ORGANISM: Candida tropicalis
US-09-911-781-24

Query Match 57.8%; Score 37; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DREFLLGF 12
|||:||||
DB 175 DREFVIGF 182

RESULT 6

US-10-400-902-24
Sequence 24, Application US/10400902
Patent No. 6790640
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Elrich, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAP (1010-49)
CURRENT APPLICATION NUMBER: US/10/400.902
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US/09/911.781
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
ORGANISM: Candida tropicalis
US-10-400-902-24

Query Match 57.8%; Score 37; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DREFLLGF 12
|||:||||
DB 175 DREFVIGF 182

```
RESULT 7
5204252-2
; Patent No. 5204252
; APPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
; PICALAGGIO, STEPHEN
; TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/386,837
; FILING DATE: 27-JUL-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 308,481
; FILING DATE: 08-FEB-1989
; SEQ ID NO: 2:
; SEQ ID NO: 2:
5204252-2

Query Match
Best Local Similarity 57.8%; Score 37; DB 6; Length 267;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DREFLGF 12
DB 175 DREFVIGF 182

RESULT 8
5204252-4
; Patent No. 5204252
; APPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
; PICALAGGIO, STEPHEN
; TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/386,837
; FILING DATE: 27-JUL-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 308,481
; FILING DATE: 08-FEB-1989
; SEQ ID NO: 4:
; SEQ ID NO: 4:
; LENGTH: 268
5204252-4

Query Match
Best Local Similarity 57.8%; Score 37; DB 6; Length 268;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DREFLGF 12
DB 176 DREFVIGF 183

RESULT 9
US-09-270-767-40048
; Sequence 40048, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40048
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURES:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40048
```

```
Query Match
Best Local Similarity 57.8%; Score 37; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RYDREFLGF 11
DB 66 RYDRSILGF 74

RESULT 10
US-09-270-767-55264
; Sequence 55264, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55264
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURES:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55264

Query Match
Best Local Similarity 57.8%; Score 37; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RYDREFLGF 11
DB 66 RYDRSILGF 74

RESULT 11
US-09-902-540-14261
; Sequence 14261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; FILING DATE: 2001-07-10
; PRIORITY APPLICATION NUMBER: 60/217,883
; FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14261
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14261

Query Match
Best Local Similarity 57.8%; Score 37; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRYDREFL 10
DB 120 KSFDRREFL 128

RESULT 12
US-08-954-333-7
; Sequence 7, Application US/08954333
```

Patent No. 5986080
GENERAL INFORMATION:
APPLICANT: Ikubo Masuda, et al.
TITLE OF INVENTION: CLONED NUCLEOTIDE PYROPHOSPHORYLALASE AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,333
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryser, David G.
REGISTRATION NUMBER: 36,407
REFERENCE/DOCKET NUMBER: 650053.91070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5717
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-954-333-7

Query Match 57.8%; Score 37; DB 1; Length 599;
Best Local Similarity 63.6%; Pred. No. 82;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KRYDREFLIG 11
|||:|:|:|
Db 138 KRREDRTFLVG 148

RESULT 13
US-09-248-796A-19839
Sequence 19839, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19839
LENGTH: 602
TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (602)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
US-09-248-796A-19839

Query Match 57.8%; Score 37; DB 2; Length 602;
Best Local Similarity 58.3%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KRYDREFLIG 12
|||:|:|:|
Db 125 KRYDREFLIG 136

RESULT 14
US-09-489-039A-8459
Sequence 8459, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8459
LENGTH: 451
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8459

Query Match 56.2%; Score 36; DB 2; Length 451;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YDREFLIG 11
|||:|:|:|
Db 265 YDREFLIG 272

RESULT 15
US-09-270-767-58606
Sequence 58606, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58606
LENGTH: 55
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-58606

Query Match 54.7%; Score 35; DB 2; Length 55;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KRYDREFL 10
|||:|:|:|
Db 34 KRYDREFL 43

Search completed: November 29, 2005, 23:04:21
Job time : 30.6364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:35:04 ; Search time 115.091 Seconds
(without alignments)
73.562 Million cell updates/sec

Title: US-10-019-198a-1
Perfect score: 64
Sequence: 1 KKRYDREFLGLF 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	175	2 Q6EVH7_RABIT	Q6EVH7 oryctolagus
2	64	100.0	175	2 Q6EVH8_PIG	Q6EVH8 sus scrofa
3	64	100.0	175	2 Q6EV10_HORSE	Q6EV10 equus caball
4	64	100.0	175	2 Q6EV12_BOVIN	Q6EV12 bos taurus
5	64	100.0	175	2 Q6EV13_SHEEP	Q6EV13 ovis aries
6	64	100.0	175	2 Q6EV11_MESAU	Q6EV11 mesocricetu
7	64	100.0	175	2 Q6EVH9_MOUSE	Q6EVH9 mus musculu
8	64	100.0	1402	1 IFAG1_RABIT	P41110 oryctolagus
9	64	100.0	1423	2 Q7YSJ5_FELCA	Q7YSJ5 felis silve
10	64	100.0	1600	1 IFAG1_HUMAN	O04637 homo sapien
11	64	100.0	1600	1 IFAG1_MOUSE	O6nrj6 mus musculu
12	64	100.0	1624	2 Q4LE58_HUMAN	Q4LE58 homo sapien
13	61	95.3	1815	2 Q4RYZ6_TETNG	Q4RYZ6 tetraodon n
14	53	82.8	247	2 Q5SMD1_HUMAN	O5swd1 homo sapien
15	53	82.8	308	2 Q4R3V6_MACFA	Q4R3V6 macaca fasc
16	53	82.8	1305	2 Q504Z1_HUMAN	O504z1 homo sapien
17	53	82.8	1585	1 IFAG3_HUMAN	O43432 homo sapien
18	53	82.8	1585	2 Q5SNC3_HUMAN	O5snc3 homo sapien
19	53	82.8	1623	2 Q6RX22_HORSE	Q6RX22 equus caball
20	53	82.8	1780	2 Q59GJ0_HUMAN	Q59GJ0 homo sapien
21	50	78.1	1610	2 Q4T9L8_TETNG	Q4T9L8 tetraodon n
22	49	76.6	1745	2 Q6AZ82_SPHRG	Q6az82 sphaerechin
23	48	75.0	1578	2 Q6GCV5_MOUSE	Q6gcv5 mus musculu
24	48	75.0	1579	1 IFAG3_MOUSE	O80x13 mus musculu
25	46	71.9	569	2 Q88VK1_LACPL	Q88VK1 lactobacilli
26	46	71.9	1203	2 Q55ZY6_CRYNE	Q55ZY6 cryptococcu
27	46	71.9	1203	2 Q5KP94_CRYNE	Q5KP94 cryptococcu
28	46	71.9	1494	2 Q55ZW9_CRYNE	Q55ZW9 cryptococcu
29	46	71.9	1494	2 Q5K788_CRYNE	Q5K788 cryptococcu
30	45	70.3	733	2 Q4T2D5_TETNG	Q4T2D5 tetraodon n
31	45	70.3	1740	2 Q4P632_USTMA	Q4P632 ussilaigo ma

32	44	68.8	553	2	Q25496_HELPY	Q25496 helicobacte
33	44	68.8	553	2	Q9Z124_HELBJ	Q9Z124 helicobacte
34	42	65.6	363	2	Q6ESR6_ORYSA	Q6ESR6 oryza sativ
35	41	64.1	572	2	Q4FUL6_GAMMA	Q4FUL6 psychrobact
36	41	64.1	674	2	Q7U9R3_SYNXP	Q7U9R3 synecococc
37	40	62.5	277	2	Q58047_PYRHO	Q58047 pyrococcus
38	40	62.5	468	1	BMP3_RAT	P49002 rattus norv
39	40	62.5	750	2	Q59G53_HUMAN	Q59G53 homo sapien
40	40	62.5	1318	2	Q4RRG9_TETNG	Q4RRG9 tetraodon n
41	40	62.5	1401	2	Q9LKG7_ARYSA	Q9LKG7 arabidopsis
42	40	62.5	1501	2	Q69S49_ORYSA	Q69S49 oryza sativ
43	40	62.5	1606	2	Q9LYJ9_ARYTH	Q9LYJ9 arabidopsis
44	40	62.5	1725	2	Q76E23_ARYTH	Q76E23 arabidopsis
45	40	62.5	3052	2	Q5T0X9_HUMAN	Q5T0X9 homo sapien

ALIGNMENTS

```

RESULT 1
ID Q6EVH7_RABIT PRELIMINARY; PRT; 175 AA.
AC Q6EVH7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE EIF4G1 protein (fragment).
GN Name=EIF4G1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;
RA Strong R., Belsham G.J.;
RT "Sequential modification of translation initiation factor eIF4G1 by
RT two different foot-and-mouth disease virus proteases within infected
RT BHK cells; identification of the 3Cpro cleavage site.";
RL J. Gen. Virol. 85:2953-2962(2004).
DR EMBL: AJ746224; CAC34104.1; -, mRNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 175 AA; 19399 MW; C53979B9BA79CCCB CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRYDREFLGLF 12
   |||||
DB 6 KKRYDREFLGLF 17

RESULT 2
ID Q6EVH8_PIG PRELIMINARY; PRT; 175 AA.
AC Q6EVH8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE EIF4G1 protein (fragment).
GN Name=EIF4G1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sui.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;
RA Strong R., Belsham G.J.;

```

RT "Sequential modification of translation initiation factor eIF4GI by
RT two different foot-and-mouth disease virus proteases within infected
RT BHK cells; identification of the 3Cpro cleavage site."
RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746223; CAG34103.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19484 MW; A1B7201B128AC731 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

RESULT 3

Q6EV10 HORSE
ID Q6EV10 HORSE PRELIMINARY; PRT; 175 AA.

AC Q6EV10; 28, Created

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE EIF4GI protein (Fragment).

OS Name-eIF4GI;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

OC NCBI_TaxID=9796;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=lung;

RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;

RA Strong R., Belsham G.J.;

RT "Sequential modification of translation initiation factor eIF4GI by

RT two different foot-and-mouth disease virus proteases within infected

RT BHK cells; identification of the 3Cpro cleavage site."

RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746221; CAG34101.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19494 MW; 1AAACF151D93D73C CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

RESULT 4

Q6EV12 BOVIN
ID Q6EV12 BOVIN PRELIMINARY; PRT; 175 AA.

AC Q6EV12; 28, Created

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE EIF4GI protein (Fragment).

OS Name-eIF4GI;

OC Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;

RA Strong R., Belsham G.J.;

RT "Sequential modification of translation initiation factor eIF4GI by

RT two different foot-and-mouth disease virus proteases within infected

RT BHK cells; identification of the 3Cpro cleavage site."

RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746221; CAG34101.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19494 MW; 1AAACF151D93D73C CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

RT two different foot-and-mouth disease virus proteases within infected
RT BHK cells; identification of the 3Cpro cleavage site."

RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746219; CAG34099.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19486 MW; A1BF7004028DC72D CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

RESULT 5

Q6EV13 SHEEP
ID Q6EV13 SHEEP PRELIMINARY; PRT; 175 AA.

AC Q6EV13; 28, Created

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE EIF4GI protein (Fragment).

OS Name-eIF4GI;

OC Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Caprinae; Ovis.

OC NCBI_TaxID=9940;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;

RA Strong R., Belsham G.J.;

RT "Sequential modification of translation initiation factor eIF4GI by

RT two different foot-and-mouth disease virus proteases within infected

RT BHK cells; identification of the 3Cpro cleavage site."

RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746218; CAG34098.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19486 MW; A1BF7004028DC72D CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

RESULT 6

Q6EV11 MESAU
ID Q6EV11 MESAU PRELIMINARY; PRT; 175 AA.

AC Q6EV11; 28, Created

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE EIF4GI protein (Fragment).

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Cricetinae; Mesocricetus.

OC NCBI_TaxID=10036;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;

RA Strong R., Belsham G.J.;

RT "Sequential modification of translation initiation factor eIF4GI by

RT two different foot-and-mouth disease virus proteases within infected

RT BHK cells; identification of the 3Cpro cleavage site."

RL J. Gen. Virol. 85:2953-2962(2004).

DR EMBL: AJ746218; CAG34098.1; -; mRNA.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 175 AA; 19486 MW; A1BF7004028DC72D CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKKRYDRFFLLGF 12
Db 6 KKKRYDRFFLLGF 17

```

RT two different foot-and-mouth disease virus proteases within infected
RT BHK cells; identification of the 3Cpro cleavage site.";
RL J. Gen. Virol. 85:2953-2962(2004).
DR EMBL; AJ746220; CAG34100.1; -, mRNA.
FT NON_TER 1
FT NON_TER 175
SQ SEQUENCE 175 AA; 19562 MW; 4E4FA478030256EA CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDREFLGF 12
DB 6 KRRYDREFLGF 17

RESULT 7
Q6EVH9 MOUSE PRELIMINARY; PRT; 175 AA.
Q6EVH9
AC 06EVH9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE E1F4G1 protein (Fragment).
GN Name=E1f4g1; Synonym=e1f4g1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448358; DOI=10.1099/vir.0.80254-0;
RA Strong R., Beishan G.J.;
RT "Sequential modification of translation initiation factor e1f4g1 by
RT two different foot-and-mouth disease virus proteases within infected
RT BHK cells; identification of the 3Cpro cleavage site.";
RL J. Gen. Virol. 85:2953-2962(2004).
DR EMBL; AJ746222; CAG34102.1; -, mRNA.
DR MGI; MGI:2384784; E1f4g1.
DR GO; GO:0005737; Cytoplasm; IDA.
FT NON_TER 1
FT NON_TER 175
SQ SEQUENCE 175 AA; 19532 MW; EC221DC60B116AE CRC64;

Query Match 100.0%; Score 64; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDREFLGF 12
DB 6 KRRYDREFLGF 17

RESULT 8
IF4G1 RABIT STANDARD; PRT; 1402 AA.
IF4G1
AC P41110;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Eukaryotic translation initiation factor 4 gamma 1 (e1f-4-gamma 1)
DE (e1f-4g1) (e1f-4g 1) (p220).
GN Name=IF4G1; Synonym=e1f4g;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 479-500.
RC STRAIN=New Zealand white; TISSUE=Brain;

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RX MEDLINE=93374895; PubMed=8396129;
RA Lamphear B.J., Yan R., Yang F., Waters D., Liebig H.-D., Klump H.,
RA Kuechler E., Skern T., Rhoads R.E.;
RT "Mapping the cleavage site in protein synthesis initiation factor e1f-
RT 4 gamma of the 2A proteases from human Coxsackievirus and
RT rhinovirus.";
RL J. Biol. Chem. 268:19200-19203(1993).
RN [2]
RP PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=93054654; PubMed=1429670;
RA Yan R., Rychlik W., Etchison D., Rhoads R.E.;
RT "Amino acid sequence of the human protein synthesis initiation factor
RT e1f-4 gamma.";
RL J. Biol. Chem. 267:23226-23231(1992).
CC -1- FUNCTION: Component of the protein complex e1f4F, which is
CC INVOLVED in the recognition of the mRNA cap, ATP-dependent
CC unwinding of 5'-terminal secondary structure and recruitment of
CC mRNA to the ribosome.
CC -1- SUBUNIT: e1f4F is a multi-subunit complex, the composition of
CC which varies with external and internal environmental conditions.
CC It is composed of at least E1F4A, E1F4B and E1F4G1/E1F4G3.
CC It interacts with e1f3, mutually exclusive with E1F4I or E1F4J,
CC E1F4B and through its N-terminus with PAPB1. Interacts through
CC its C-terminus with the serine/threonine kinases MNK1, and with
CC MNK2. Appears to act as a scaffold protein, holding these enzymes
CC in place to phosphorylate E1F4E (By similarity).
CC -1- SIMILARITY: Belongs to the e1f4G family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L22090; AAA31242.1; -, mRNA.
CC PIR; I46707; I46707.
CC HSSP; 043432; 1HU3.
CC DR P41110; 1036-1367.
CC DR SMR; P41110; 1036-1367.
CC DR InterPro; IPR003307; e1f5C.
CC DR InterPro; IPR003890; IF_e1f4G.
CC DR InterPro; IPR003891; IF_e1f4G_MA3.
CC DR Pfam; PF02847; MA3; 1.
CC DR Pfam; PF02854; M1F4G; 1.
CC DR Pfam; PF02020; W2; 1.
CC DR Pfam; SM00515; e1f5C; 1.
CC DR SMART; SM00544; MA3; 1.
CC DR SMART; SM00543; M1F4G; 1.
CC DR Direct protein sequencing; Initiation factor; Phosphorylation;
CC Protein biosynthesis; RNA-binding; Translation regulation.
CC KW COMBIAS 188 192 Poly-Pro.
CC FT COMBIAS 262 275 Poly-Glu.
CC FT COMBIAS 1393 1398 Poly-Glu.
CC FT MOD_RES 1012 1012 Phosphoserine (By similarity).
CC FT MOD_RES 1034 1034 Phosphoserine (By similarity).
CC FT SEQUENCE 1402 AA; 154051 MW; 7FD85D7B30519230 CRC64;

Query Match 100.0%; Score 64; DB 1; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDREFLGF 12
DB 414 KRRYDREFLGF 425

RESULT 9
Q7S39_FELCA PRELIMINARY; PRT; 1423 AA.
Q7S39
AC Q7S39;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eukaryotic translation initiation factor 4G1 (Fragment).

```



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RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mitaide I., Osero N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldevelil R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirfl L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Bruesel V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregant T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guerinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kanesawa Y., Kedzierski R.W., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhart B., Lyons P.A.,
RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
RA Naashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Borje A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Zennaro P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Component of the protein complex eIF4F, which is
CC involved in the recognition of the mRNA cap, ATP-dependent
CC unwinding of 5'-terminal secondary structure and recruitment of
CC mRNA to the ribosome (By similarity).
CC -1- SUBUNIT: eIF4F is a multi-subunit complex, the composition of
CC which varies with external and internal environmental conditions.
CC It is composed of at least eIF4A, eIF4E and eIF4G/eIF4G3.
CC eIF4E interacts with eIF3, mutually exclusive with eIF4A or eIF4G,
CC eIF4E and through its N-terminus with PAPB1. Interacts through
CC its C-terminus with the serine/threonine kinases MNK1, and with
CC MNK2. Appears to act as a scaffold protein, holding these enzymes
CC in place to phosphorylate eIF4E. Non-phosphorylated eIF4EBP1
CC competes with eIF4G/eIF4G3 to interact with eIF4E; insulin
CC stimulated MAP-kinase (MAPK1 and MAPK3) phosphorylation of
CC eIF4EBP1 causes dissociation of the complex allowing eIF4G/eIF4G3
CC to bind and consequent initiation of translation (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q6NZJ6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q6NZJ6-2; Sequence=VSP_013974, VSP_013975;
CC -1- SIMILARITY: Belongs to the eIF4G family.
CC -1- SIMILARITY: Contains 1 MIF4G domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BC066038; AAH66038.1; -; mRNA.
CC EMBL; BC066103; AAH66103.1; -; mRNA.
CC EMBL; BC079675; AAH79675.1; -; mRNA.
CC EMBL; AK053144; BAC35282.1; -; mRNA.
CC SMK; Q6NZJ6; 755-995, 1234-1565.
CC EMBL; ENSMUSG0000045983; Mus musculus.
CC MGI; MGI:2384784; Eif4g1.
CC GO; GO:0005737; Cytoplasm; IDA.
CC InterPro; IPR003307; eIF5C.
CC InterPro; IPR003890; IF_eIF4G.
CC InterPro; IPR003891; IF_eIF4G_MA3.
CC Pfam; PF02847; MA3; 1.

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DR Pfam; PF02854; MIF4G; 1.
DR Pfam; PF02020; W2; 1.
DR SMART; SM00515; eIF5C; 1.
DR SMART; SM00544; MA3; 1.
DR SMART; SM00543; MIF4G; 1.
KW Alternative splicing; Initiation factor; Phosphorylation;
KW Protein biosynthesis; RNA-binding; Translation regulation.
FT DOMAIN 765 993
FT REGION 179 207
FT REGION 611 622
FT REGION 686 1089
FT REGION 1450 1600
FT REGION 1585 1600
FT COMPB1AS 464 487
FT MOD_RES 1211 1211
FT MOD_RES 1231 1231
FT VARSP1IC 49 55
FT VARSP1IC 1046 1052
SQ SEQUENCE 1600 AA; 176077 MW; 8664AB44C7A128 CRC64;
Query Match 100.0%; Score 64; DB 1; Length 1600;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKRYDRFFLG 12
Db 613 KKRYDRFFLG 624
RESULT 12
Q4LE58 HUMAN PRELIMINARY; PRT; 1624 AA.
AC Q4LE58;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE eIF4G1 variant protein (Fragment).
GN Name=eIF4G1 variant protein;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Eumetazoa; Chordata; Vertebrata; Euteleostomi;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,
RA Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;
RT "Preparation of a set of expression-ready clones of mammalian long
RT cDNAs encoding large proteins by the ORF trap cloning method."
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB310013; BA806095.1; -; mRNA.
FT NON_TER 1
FT SEQUENCE 1624 AA; 178155 MW; 60018B9790D1710F CRC64;
Query Match 100.0%; Score 64; DB 2; Length 1624;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKRYDRFFLG 12
Db 634 KKRYDRFFLG 645
RESULT 13
Q4RYZ6 TETNG PRELIMINARY; PRT; 1615 AA.
AC Q4RYZ6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:35:24 ; Search time 18.8182 Seconds
(without alignments)
61.356 Million cell updates/sec

Title: US-10-019-198a-1
Perfect score: 64
Sequence: 1 KKRYDREFLLGF 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	1402	2	146707 translation initia
2	52.5	82.0	1396	2	A44453 osmoprotection pro
3	44	68.8	553	2	B64622 probable osmoprote
4	44	68.8	553	2	G71892 hypothetical prote
5	40	62.5	277	2	G71456 bone morphogenetic
6	40	62.5	360	2	I53032 translation initia
7	40	62.5	1606	2	T49219 DNA-directed DNA p
8	40	62.5	3122	2	T17202 dipeptidase BH2271
9	39	60.9	310	2	G83933 probable translati
10	39	60.9	1666	2	T09072 rep protein - Cory
11	38	59.4	332	2	I40726 hypothetical prote
12	37.5	58.6	1418	2	S64918 hypothetical prote
13	37	57.8	212	2	D64133 hypothetical prote
14	37	57.8	320	2	G72629 prolyl-tRNA synthe
15	37	57.8	570	2	C81094 proline-tRNA ligas
16	37	57.8	570	2	D81847 heat shock protein
17	37	57.8	611	2	A75080 hypothetical prote
18	37	57.8	581	2	A85000 hypothetical prote
19	37	57.8	673	2	T46340 hypothetical prote
20	37	57.8	1018	2	T47300 hypothetical prote
21	37	57.8	2142	2	D86303 P17P16.1 protein -
22	36	56.2	102	2	S29532 hypothetical prote
23	36	56.2	172	2	S73542 MG428 homolog C12
24	36	56.2	309	2	G69726 tRNA-pseudouridine
25	36	56.2	348	2	S47841 lipopolysaccharide
26	36	56.2	348	2	B91191 ADP-hepseose-1ps he
27	36	56.2	348	2	C86038 ADP-hepseose-1ps he
28	36	56.2	364	2	S28612 catechol O-methyl
29	36	56.2	426	2	G36891 transfer complex p

30	36	56.2	435	2	AB0453 isocitrate lyase (
31	36	56.2	5369	2	T44807 mycosubtilin synth
32	35.5	55.5	86	2	D86774 transposase [impor
33	35.5	55.5	86	2	A86781 transposase [impor
34	35.5	55.5	86	2	B86636 probable phenylala
35	35.5	55.5	468	2	S75389 MHC class II alpha
36	35	54.7	71	2	I51749 hypothetical prote
37	35	54.7	124	2	B87345 small heat shock p
38	35	54.7	176	2	D90414 hypothetical prote
39	35	54.7	177	2	S45412 L-fuculose-phospha
40	35	54.7	181	1	A64477 hypothetical prote
41	35	54.7	265	2	C83685 oroticidine-5'-phosp
42	35	54.7	266	1	JS0721 probable polynucle
43	35	54.7	294	2	D82371 hypothetical prote
44	35	54.7	300	2	P84594 ER calcium-binding
45	35	54.7	317	2	I37371

ALIGNMENTS

RESULT 1
146707
translation initiation factor eIF4-gamma - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146707
R:Yan, R.; He, W.; Rhoads, R.E.
J. Biol. Chem. 268, 19200-19203, 1993
A:Title: Mapping the cleavage site in protein synthesis initiation factor eIF-4 gamma of
A:Reference number: 146707; MUID:93374895; PMID:8396129
A:Accession: 146707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1402 <YAN>
A:Cross-references: UNIPROT:P41110; UNIPARC:UPI000012D372; GB:I22090; NID:5404774; PIDN:

Query Match 100.0%; Score 64; DB 2; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRYDREFLLGF 12
DB 414 KKRYDREFLLGF 425

RESULT 2

A44453
translation initiation factor eIF-4 gamma - human

C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994

C:Accession: A44453

R:Yan, R.; Rychlik, W.; Etchison, D.; Rhoads, R.E.
J. Biol. Chem. 267, 23226-23231, 1992

A:Title: Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma

A:Reference number: A44453; MUID:93054654; PMID:1428670

A:Accession: A44453

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-1396 <YAN>

A:Cross-references: UNIPARC:UPI000017C3F3

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBI:P118286)

Query Match 82.0%; Score 52.5; DB 2; Length 1396;
Best Local Similarity 80.0%; Pred. No. 0.13;
Matches 12; Conservative 0; Mismatches 3; Indels 1;

QY 1 KKRYDREFLLGF 12
DB 410 KKRYDREFLLGF 424

RESULT 3

osmoprotection protein - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C/Accession: B64622
R/Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalek, H.G.; Glodet, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Meldrum, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: B64622
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-553 <TOM>
C/GenBank-references: UNIPROT:O25496; UNIPARC:UPI00000D313B; GB:AEO00593; GB:AEO00511; NITD

Q

Query Match	68.8%	Score 44	DB 2	Length 553
Best Local Similarity	55.6%	Pred. No. 2		
Matches 10	Conservative 2	Mismatches 0	Indels 6	Gaps 1
Qy	1 KKRYPREF-----LLGF 12			
	::			
db	369 KKRYPEKENLLLVGILGF 386			

RESULT 4

Probable omoprotection binding protein - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: G71892
R:Alt, R.A.; Ling, R.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, L.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho-
A:Reference number: A1800; MUID:99120557; PMID:9923682
A:Accession: G71892
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-553 <ARN>
A:Cross-references: UNIPROT:Q9ZL24; UNIPARC:UPI00000D3696; GB:AE001506; GB:AE001439; NITD
A:Experimental source: strain J99
C:Genetics:
C:Gene: jhp0757

Q

Query Match	68.8%	Score 44	DB 2	Length 553
Best Local Similarity	55.6%	Pred. No. 2		
Matches	10	Conservative	2	Mismatches 0
				Indels 6
				Gaps 1
Qy	1	KKRYDREF-----LLGF	12	
		::		
db	369	KKRYEKENLLMVGLGF	386	

RESULT 5

hypothetical protein PH0309 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: G71456
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.
DNA Rep. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71456
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-277 <KAW>

A1:Cross-references: UNIPROT:O58047; UNIPARC:UPI000000629D6; GB:AP000001; NID:g3236128; Pfl
A1:Experimental source: strain OT3
A1:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A1:Gene: PH0309

Q

Query Match	62.5%	Score 40	DB: 2	Length 277
Best Local Similarity	72.7%	Pred. No. 5	7	
Matches	8	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
QY	2	KRYDREFLLGF	12	
DB	158	KAYDREFLLKGF	168	

RESULT 6

bone morphogenetic protein 3 - rat (fragment)
C|Species: Rattus sp. (rat)
C|Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C|Accession: I53032
R|Chan, D.; Feng, Y.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.
DNA Cell Biol. 14, 235-239, 1995
A|Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cultu
A|Reference number: I53032; MUID:95186061; PMID:7880444
A|Accession: I53032
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-360 <RES>
A|Cross-references: UNIPARC:UPI0000170CBA; GB:S77492; NID:957225; PIDN:AAB33725.1; PID4
C|Superfamily: Inhib

Q

Query Match	62.5%	Score 40;	DB 2;	Length 360;
Best Local Similarity	58.3%	Pred. No. 7.6;		
Matches	7;	Conservative	2;	Mismatches 3; Indels 0; Gaps 0;
QY	1	KKRYDREPLFG	12	
	:			
Db	96	KAKQDEEFLFG	107	

RESULT 7

translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - Arabidopsis chr4
 M1:Alternate names: protein F27H5.30
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T49219
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, April 2000
 A:Accession: T49219
 A:Reference number: 225018
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1606 <RIE>
 A:Cross-references: UNIPROT:O9LY39; UNIPARC:UPI000009C67C; EMBL:ALJ63852; GSPDB:GN00061;
 A:Experimental source: cultivar Columbia; BAC clone F27H5
 C:Genetics:
 A:Gene: AISP:F27H5.30
 A:Map position: 3
 A:Introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2

Q

	Query Match	62.5%	Score 40;	DB 2;	Length 1606;
	Best Local Similarity	58.3%;	Pred. No. 41;		
Matches	7; Conservative	3;	Mismatches	2;	Indels 0;
Gaps	0;				
QY	1 KKKRYDREFLLGF	12			
	: : : : :				
Db	734 EKKYSRDFFLKF	745			

RESULT 8

T17202

DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: F17202
R:Van Sloun, P.P.H.; Romelijn, R.J.; Eiken, J.C.J.
M:Van, R. 433, 109-116, 1999
A:Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev1 gene
A:Reference number: 218720; MUID:99202265; PMID:10102037
A:Accession: F17202
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3122 <VAN>
A:Cross-references: UNIPROT:Q61493; UNIPARC:UPI0000028721; EMBL:AF083464; NID:g4079830;
A:Experimental source: strain 129/Ola; testis
C:Genetics:
A:Map position: 10
C:Keywords: nucleotidyltransferase

Query Match 62.5%; Score 40; DB 2; Length 3122;
Best Local Similarity 63.6%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRYDREPLGF 12
|||:||||:
Db 2386 KRYDREPLGF 2396

RESULT 9
diPeptidase BH2271 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83933
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: UNIPROT:Q9KAL6; UNIPARC:UPI000000356A; GB:AF001515; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2271
C:Superfamily: membrane dipeptidase

Query Match 60.9%; Score 39; DB 2; Length 310;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KRYDREPLGF 12
|||:||||:
Db 286 KRYDREPLGF 296

RESULT 10
T09072
probable translation initiation factor eIF-4 gamma - fruit fly (Drosophila melanogaster)
N:Alternate names: translation initiation factor eIF4G
C:Species: Drosophila melanogaster
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09072
R:Hernandez, G.; Castellano, M.M.; Agudo, M.; Sierra, J.M.
Eur. J. Biochem. 253, 27-35, 1998
A:Title: Isolation and characterization of the cDNA and the gene for eukaryotic translat
A:Reference number: Z15553; MUID:98237569; PMID:9578457
A:Accession: T09072
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-166 <HER>
A:Cross-references: UNIPROT:Q61380; UNIPARC:UPI000007DECF; EMBL:AF030155; NID:g3056722;
A:Experimental source: strain Oregon R

C:Genetics:
A:Cross-references: Flybase:FBgn0023213
A:Map position: 4
C:Keywords: protein biosynthesis

Query Match 60.9%; Score 39; DB 2; Length 1666;
Best Local Similarity 80.0%; Pred. No. 66;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCRYDREPL 10
|||:||||:
Db 618 KCRYDREPL 627

RESULT 11
I40726
rep protein - Corynebacterium glutamicum
C:Species: Corynebacterium glutamicum
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40726
R:Archer, J.A.; Sinskey, A.J.
J. Gen. Microbiol. 139, 1753-1759, 1993
A:Title: The DNA sequence and minimal replicon of the Corynebacterium glutamicum plasmid
A:Reference number: I40726; MUID:94014972; PMID:8409918
A:Accession: I40726
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-332 <RES>
A:Cross-references: UNIPROT:Q46071; UNIPARC:UPI000006BEE; EMBL:Z22927; NID:g311990; PDB
C:Genetics:
A:Gene: rep
A:Start codon: GTG

Query Match 59.4%; Score 38; DB 2; Length 332;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KCRYDREPL 11
|||:||||:
Db 94 KCRYDREPL 104

RESULT 12
S64918
hypothetical protein YLR086w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein I2501
C:Species: Saccharomyces cerevisiae
C:Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: S64918; S64920
R:Polh, T.M.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64899
A:Accession: S64918
A:Molecule type: DNA
A:Residues: 1-1418 <POH>
A:Cross-references: UNIPROT:Q12267; UNIPARC:UPI000005327B; EMBL:Z73258; NID:g1360454; PDB
A:Experimental source: strain S288C
R:Benes, V.; Rehmann, S.; Nentwich, U.; Schwager, C.; Ansoerge, W.; Voss, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64920
A:Accession: S64920
A:Molecule type: DNA
A:Residues: 257-1418 <BEN>
A:Cross-references: UNIPARC:UPI0000168F70; EMBL:Z73258; MIPS:YLR086w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:SMC4
A:Cross-references: SGD:S0004076
A:Map position: 12R
C:Superfamily: chromosome segregation protein SMC1

Query Match 58.6%; Score 37.5; DB 2; Length 1418;
Best Local Similarity 66.7%; Pred. No. 11e+02;

Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 KKYDREFLGF 12

Db 1261 KKRPD-EFMAGP 1271

RESULT 13

D64133
hypothetical protein H11629 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C/Accession: D64133

R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervatage, A.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: D64133

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-212 <TIGR>

A/Cross-references: UNIPROT:P45280; UNIPARC:UPI000013AF4F; GB:U32836; GB:L42023; NID:915

C/Genetics:

A/Start codon: GTG

C/Superfamily: probable alkaline phosphatase yngC

Query Match 57.8%; Score 37; DB 2; Length 212;

Best Local Similarity 58.3%; Pred. No. 16;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKYDREFLGF 12

Db 13 KKOQMEFLGF 24

RESULT 14

G72629
hypothetical protein APE1495 - Aeropyrum pernix (strain K1)

C/Species: Aeropyrum pernix

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004

C/Accession: G72629

R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahawa, H.; Takamitsu, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A/Reference number: A72450; MUID:99310339; PMID:10382366

A/Accession: G72629

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-320 <KAW>

A/Cross-references: UNIPROT:Q9YBV5; UNIPARC:UPI000005DF8A; DDBJ:AP000061; NID:95104821;

C/Genetics:

A/Experimental source: strain K1

A/Gene: APE1495

Query Match 57.8%; Score 37; DB 2; Length 320;

Best Local Similarity 75.0%; Pred. No. 26;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKYDREFL 9

Db 83 RRYDREYL 90

RESULT 15

C81094
prolyl-tRNA synthetase NMB1339 [imported] - Neisseria meningitidis (strain MC58 serogroup

C/Species: Neisseria meningitidis

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: C81094

R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizsa, M. Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A/Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: C81094

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-570 <TET>

A/Cross-references: UNIPROT:Q9J214; UNIPARC:UPI00000C46B1; GB:AE002482; GB:AE002098; NID:

A/Experimental source: serogroup B, strain MC58

C/Genetics:

A/Gene: NMB1339

C/Superfamily: proline-tRNA ligase

Query Match 57.8%; Score 37; DB 2; Length 570;

Best Local Similarity 54.5%; Pred. No. 49;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKYDREFLGF 11

Db 97 KKHDRDFCWG 107

Search completed: November 29, 2005, 23:02:30
Job time : 20.8182 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: November 29, 2005, 21:58:13 ; Search time 114.545 Seconds
(without alignments)
46.030 Million cell updates/sec

Title: US-10-019-198a-1
Perfect score: 64
Sequence: 1 KKRYDRFLGLGF 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: geneseqp1980a:.*
2: geneseqp1990a:.*
3: geneseqp2000a:.*
4: geneseqp2001a:.*
5: geneseqp2002a:.*
6: geneseqp2003a:.*
7: geneseqp2003b:.*
8: geneseqp2004a:.*
9: geneseqp2005a:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	12	4 AAB31445	Aab31445 Peptide d
2	64	100.0	12	4 AAB31438	Aab31438 A human e
3	64	100.0	14	4 AAB31450	Aab31450 Peptide d
4	64	100.0	16	3 AAB11096	Aab11096 Human eif
5	64	100.0	16	3 AAB11100	Aab11100 Zebrafish
6	64	100.0	16	3 AAB11098	Aab11098 Rabbit ei
7	64	100.0	16	4 AAB84405	Aab84405 4E-bindin
8	64	100.0	16	4 AAB84401	Aab84401 4E-bindin
9	64	100.0	16	4 AAB84403	Aab84403 4E-bindin
10	64	100.0	30	4 AAB31443	Aab31443 Peptide d
11	64	100.0	903	8 ADR10076	ADR10076 Human pro
12	64	100.0	1395	7 ADD46044	Add46044 Human pro
13	64	100.0	1396	8 ADO19635	Ado19635 Human PRO
14	64	100.0	1396	8 ADP54731	Adp54731 Human PRO
15	64	100.0	1560	3 AAB18792	Aab18792 The human
16	64	100.0	16	3 AAB11097	Aab11097 Human eif
17	64	100.0	16	4 AAB84402	Aab84402 4E-bindin
18	64	100.0	133	7 ADD27383	Add27383 Human adi
19	64	100.0	1139	8 ADI16228	Adi16228 Human nuc
20	64	100.0	1556	8 ADQ97964	Adq97964 Human can
21	64	100.0	1584	3 AAY84430	Aay84430 Amino aci
22	64	100.0	1585	8 ADQ97962	Adq97962 Human can
23	64	100.0	1585	9 ADZ70319	Adz70319 Human pro
24	64	100.0	1756	4 ABG20440	Abg20440 Novel hum

25	48	75.0	1576	8 ADQ97959	Adq97959 Mouse can
26	45	70.3	14	4 AAB31451	Aab31451 Peptide d
27	44	68.8	226	2 AAW20422	Aaw20422 H. pylori
28	44	68.8	339	2 AAW20906	Aaw20906 H. pylori
29	42	65.6	354	7 ABM86083	Abm86083 Rice abio
30	40	62.5	941	8 ADI45381	Adi45381 Rice isop
31	40	62.5	1725	7 ADC54131	Adc54131 Eukaryoti
32	40	62.5	2479	7 ADK40962	Adk40962 Novel hum
33	40	62.5	2479	8 ADR15681	Adr15681 Kinase 69
34	40	62.5	2872	8 ADR46703	Adr46703 Cancer-as
35	40	62.5	3052	9 ADX07307	Adx07307 Cyclin-de
36	40	62.5	3173	7 ADE09433	Ado9433 Novel pro
37	40	62.5	3173	7 ADE09353	Ado9353 Novel pro
38	39	60.9	16	3 AAB11101	Aab11101 Drosophi
39	39	60.9	16	4 AAB84406	Aab84406 4E-bindin
40	39	60.9	310	8 ADS28271	Ads28271 Bacterial
41	39	60.9	543	6 ADB10596	Adb10596 Altiolococ
42	39	60.9	568	6 ADB10594	Adb10594 Altiolococ
43	39	60.9	571	6 ADB10592	Adb10592 Altiolococ
44	39	60.9	1666	4 ABB72054	Abb72054 Drosophi
45	38	59.4	79	2 AAY59752	Aay59752 Human nor

ALIGNMENTS

RESULT 1
AAB31445
ID AAB31445 standard; peptide; 12 AA.

AC AAB31445;

DT 20-APR-2001 (first entry)

DE Peptide derived from human eukaryotic Initiation Factor 4G (eIF4G).

KW Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
cell death; cell apoptosis; anticancer; antitumor.

OS Homo sapiens.

PN WO200078803-A2.

PD 28-DEC-2000.

XX 21-JUN-2000; 2000WO-GB002414.

XX 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

PA Proud CG, Herbert TP, Lane DP, Fahraeus R;

PI WPI; 2001-071386/08.

PT Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
for inducing apoptosis in e.g. mammalian tumor cells.

XX Example; Fig 5; 46pp; English.

PS The present sequence represents a peptide derived from an eukaryotic
XX Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
XX and eIF4E binding agents, such as peptides or peptidomimetics. These
XX binding agents are used for the induction of cell death. The binding
XX peptides are used for inducing cell apoptosis. They are used in
XX pharmaceutical compositions for anticancer or antitumor treatment of
XX mammalian cells. Specifically, the peptides result in growth inhibition
XX of, or increased cytotoxicity to, tumour cells

SO Sequence 12 AA;

Query Match 100.0%; Score 64; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 9,7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRYDRFLGLF 12
| | | | | | | | | |
Db 1 KRRYDRFLGLF 12

RESULT 2

AAB31438 ID AAB31438 standard; peptide; 12 AA.

XX AAB31438;

XX 20-APR-2001 (first entry)

XX A human eukaryotic Initiation Factor 4G (eIF4G) binding peptide.

XX Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;

KM cell death; cell apoptosis; anticancer; antitumor.

XX Homo sapiens.

XX MO200078803-A2.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000MO-GB002414.

XX 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

XX Proud CG, Herbert TP, Lane DP, Fahraeus R;

XX WPI; 2001-071386/08.

XX Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
PT binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
PT for inducing apoptosis in e.g. mammalian tumor cells.

XX Claim 6; Page 31; 46pp; English.

XX The present sequence represents a binding peptide for an eukaryotic

CC Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
CC and eIF4E binding agents, such as peptides or peptidomimetics. These
CC binding agents are used for the induction of cell death. The binding
CC peptides are used for inducing cell apoptosis. They are used in
CC pharmaceutical compositions for anticancer or antitumor treatment of
CC mammalian cells. Specifically, the peptides result in growth inhibition
CC of, or increased cytotoxicity to tumor cells

XX Sequence 12 AA;

Qy Query Match 100.0%; Score 64; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 9,7e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRYDRFLGLF 12
| | | | | | | | | |
Db 1 KRRYDRFLGLF 12

RESULT 3

AAB31450 ID AAB31450 standard; peptide; 14 AA.

XX AAB31450;

XX 20-APR-2001 (first entry)

XX Peptide derived from human eukaryotic Initiation Factor 4G (eIF4G).

KM Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
XX cell death; cell apoptosis; anticancer; antitumor.

XX Homo sapiens.

XX MO200078803-A2.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000MO-GB002414.

XX 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

XX Proud CG, Herbert TP, Lane DP, Fahraeus R;

XX WPI; 2001-071386/08.

XX Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
PT binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
PT for inducing apoptosis in e.g. mammalian tumor cells.

XX Example; Fig 6; 46pp; English.

XX The present sequence represents a peptide derived from an eukaryotic

CC Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
CC and eIF4E binding agents, such as peptides or peptidomimetics. These
CC binding agents are used for the induction of cell death. The binding
CC peptides are used for inducing cell apoptosis. They are used in
CC pharmaceutical compositions for anticancer or antitumor treatment of
CC mammalian cells. Specifically, the peptides result in growth inhibition
CC of, or increased cytotoxicity to tumor cells. note: the peptide is
CC biotinylated and linked to penetratin

XX Sequence 14 AA;

Qy Query Match 100.0%; Score 64; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRYDRFLGLF 12
| | | | | | | | | |
Db 1 KRRYDRFLGLF 12

RESULT 4

AAB11096 ID AAB11096 standard; peptide; 16 AA.

XX AAB11096;

XX 16-FEB-2001 (first entry)

XX Human eIF-4E recognition motif peptide heIF4Gf.

XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
KM knockout mutation; 4E-BP; glucose metabolism; fat metabolism; anorectic;
KM drug; anti-obesity; anti-fat deposition; anti-metabolic.

XX Homo sapiens.

XX MO200060932-A1.

XX 19-OCT-2000.

XX 07-APR-2000; 2000MO-CA000388.

XX 09-APR-1999; 99US-0128559P.

XX 02-FEB-2000; 2000US-0179743P.

XX (UYMC-) UNIV MCGILL.

PI Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
XX
XX WPI, 2000-672657/65.
DR
XX
XX Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
XX 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (1) whose
CC germ cells and somatic cells contain a knockout mutation in DNA encoding
CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
CC when compared to a control animal. The products of the invention have
CC antidiabetic and anorectic activity. The non-human transgenic animals are
CC useful as models for the investigation of lipid and glucose metabolism,
CC energy homeostasis and associated diseases. The transgenic animals are
CC also useful for selection and identification of modulators of the
CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
CC deposition disorders. The effect of the disruption of 4E-BP1 in the
CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
CC tissue growth, glucose metabolism and weight gain in an animal
XX
XX Sequence 16 AA:
SQ
Query Match 100.0%; Score 64; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRRYDREFLGF 12
DB 1 KRRYDREFLGF 12
RESULT 5
AAB11100
ID AAB11100 standard; peptide; 16 AA.
XX
XX AAB11100;
AC
XX
XX 12-SRP-2003 (revised)
DT 16-FEB-2001 (first entry)
XX
XX Zebrafish eIF-4E recognition motif peptide zeIF4G.
DE
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
XX knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
XX drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
XX Danilo rerio.
OS
XX WO200060932-A1.
PN
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000MO-CA000388.
PF
XX 09-APR-1999; 99US-0128559P.
PR 02-FEB-2000; 2000US-0179743P.
XX
XX (UYMC-) UNIV MCGILL.
PA
XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
PI WPI, 2000-672657/65.
XX
XX Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein

PT 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (1) whose
CC germ cells and somatic cells contain a knockout mutation in DNA encoding
CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
CC when compared to a control animal. The products of the invention have
CC antidiabetic and anorectic activity. The non-human transgenic animals are
CC useful as models for the investigation of lipid and glucose metabolism,
CC energy homeostasis and associated diseases. The transgenic animals are
CC also useful for selection and identification of modulators of the
CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
CC deposition disorders. The effect of the disruption of 4E-BP1 in the
CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
CC tissue growth, glucose metabolism and weight gain in an animal. (Updated
CC on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 16 AA:
SQ
Query Match 100.0%; Score 64; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRRYDREFLGF 12
DB 1 KRRYDREFLGF 12
RESULT 6
AAB1098
ID AAB1098 standard; peptide; 16 AA.
XX
XX AAB1098;
AC
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Rabbit eIF-4E recognition motif peptide heIF4G.
DE
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
XX knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
XX drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
XX Oryctolagus cuniculus.
OS
XX WO200060932-A1.
PN
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000MO-CA000388.
PF
XX 09-APR-1999; 99US-0128559P.
PR 02-FEB-2000; 2000US-0179743P.
XX
XX (UYMC-) UNIV MCGILL.
PA
XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
PI WPI, 2000-672657/65.
XX
XX Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
PT 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (1) whose
CC germ cells and somatic cells contain a knockout mutation in DNA encoding
CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding

protein 1) shows a phenotype of an altered glucose and/or fat metabolism CC
 when compared to a control animal. The products of the invention have CC
 antidiabetic and anorectic activity. The non-human transgenic animals are CC
 useful as models for the investigation of lipid and glucose metabolism, CC
 energy homeostasis and associated diseases. The transgenic animals are CC
 also useful for selection and identification of modulators of the CC
 expression and/or activity of 4E-BP1 and for screening drugs to isolate CC
 therapeutic agents which are useful as anti-obesity, anti-fat deposition CC
 disorder, anti-diabetes and anti-metabolic diseases associated with fat CC
 deposition disorders. The effect of the disruption of 4E-BP1 in the CC
 knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat CC
 tissue growth, glucose metabolism and weight gain in an animal CC

XX Sequence 16 AA;

Query Match 100.0%; Score 64; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDRFLG 12
 1 KRRYDRFLG 12

Db

RESULT 7
 AAB84405
 ID AAB84405 standard; peptide; 16 AA.

XX AAB84405;

AC 11-SEP-2003 (revised)

DT 22-AUG-2001 (first entry)

XX 4E-binding site of a zelfag protein.

XX 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;

KM cap-dependent translation initiation repressor; apoptosis;

KM translation initiation factor; elf4E; Ras; cancer.

XX Danio rerio.

XX MO200140293-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000MO-CA001465.

XX 02-DEC-1999; 99US-0168398P.

XX (UYMC-) UNIV MCGILL.

PA (MINU) UNIV MINNESOTA.

PI Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;

XX WPI; 2001-381379/40.

XX Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,
 PT useful for treating cancer or highly proliferative cells, comprises
 PT decreasing the amount of elf4F pre-initiation complex, relieving an
 PT apoptosis block.

XX Disclosure; Fig 6; 80pp; English.

XX AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is
 CC a repressor of cap-dependent translation initiation, and selectively
 CC activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-
 CC induced chemoresistance. The effects of 4E-BP1 are strictly dependent on
 CC its ability to sequester the translation initiation factor elf4E, thereby
 CC preventing its assembly into an active pre-initiation complex. The
 CC specification describes a method for inducing apoptosis in a cell in
 CC which the apoptosis pathway is inhibited. The method comprises decreasing
 CC the amount of elf4F pre-initiation complex by sequestration of elf4E,
 CC thus relieving an apoptosis block. The method is useful for modulating

CC pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-
 CC transformed cells. Thus, the method is particularly useful for treating
 CC cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion
 CC is useful for treating high proliferative cells. (Updated on 11-SEP-2003
 CC to standardise OS field)

XX Sequence 16 AA;

Query Match 100.0%; Score 64; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDRFLG 12
 1 KRRYDRFLG 12

Db

RESULT 8
 AAB84401
 ID AAB84401 standard; peptide; 16 AA.

XX AAB84401;

XX 22-AUG-2001 (first entry)

XX 4E-binding site of a elf4G protein.

XX 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;

KM cap-dependent translation initiation repressor; apoptosis;

KM translation initiation factor; elf4E; Ras; cancer.

XX Homo sapiens.

XX MO200140293-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000MO-CA001465.

XX 02-DEC-1999; 99US-0168398P.

XX (UYMC-) UNIV MCGILL.

PA (MINU) UNIV MINNESOTA.

PI Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;

XX WPI; 2001-381379/40.

XX Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,
 PT useful for treating cancer or highly proliferative cells, comprises
 PT decreasing the amount of elf4F pre-initiation complex, relieving an
 PT apoptosis block.

XX Disclosure; Fig 6; 80pp; English.

XX AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is
 CC a repressor of cap-dependent translation initiation, and selectively
 CC activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-
 CC induced chemoresistance. The effects of 4E-BP1 are strictly dependent on
 CC its ability to sequester the translation initiation factor elf4E, thereby
 CC preventing its assembly into an active pre-initiation complex. The
 CC specification describes a method for inducing apoptosis in a cell in
 CC which the apoptosis pathway is inhibited. The method comprises decreasing
 CC the amount of elf4F pre-initiation complex by sequestration of elf4E,
 CC thus relieving an apoptosis block. The method is useful for modulating
 CC pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-
 CC transformed cells. Thus, the method is particularly useful for treating
 CC cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion
 CC is useful for treating high proliferative cells

XX Sequence 16 AA;

Query Match 100.0%; Score 64; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00013; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KRRYDRFLGFP 12
DB 1 KRRYDRFLGFP 12

RESULT 9

AAB84403
ID AAB84403 standard; peptide; 16 AA.

AC AAB84403;

DT 22-AUG-2001 (first entry)

DE 4E-binding site of a elf4G1 protein.

XX 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;

KW cap-dependent translation initiation repressor; apoptosis;

KW translation initiation factor; elf4E; Ras; cancer.

XX Oryctolagus cuniculus.

OS WO200140293-A2.

PD 07-JUN-2001.

PF 01-DEC-2000; 2000WO-CA001465.

XX 02-DEC-1999; 99US-0168398P.

XX (UWMC-) UNIV MCGILL.

PA (MINU) UNIV MINNESOTA.

XX Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;

DR WPI; 2001-381379/40.

PT Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,

PT useful for treating cancer or highly proliferative cells, comprises

PT decreasing the amount of elf4F pre-initiation complex, relieving an

PT apoptosis block.

XX Disclosure; Fig 6; 80pp; English.

XX AAB84401-15 represent 4E-binding sites, 4E-binding protein 1 (4E-BP1) is

CC a repressor of cap-dependent translation initiation, and selectively

CC activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-

CC induced chemoresistance. The effects of 4E-BP1 are strictly dependent on

CC its ability to sequester the translation initiation factor elf4E, thereby

CC preventing its assembly into an active pre-initiation complex. The

CC specification describes a method for inducing apoptosis in a cell in

CC which the apoptosis pathway is inhibited. The method comprises decreasing

CC the amount of elf4F pre-initiation complex by sequestration of elf4E,

CC thus relieving an apoptotic block. The method is useful for modulating

CC pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-

CC transformed cells. Thus, the method is particularly useful for treating

CC cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion

CC is useful for treating high proliferative cells

XX Sequence 16 AA;

XX SQ

XX Query Match 100.0%; Score 64; DB 4; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 0.00013; Indels 0; Gaps 0;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 KRRYDRFLGFP 12

XX DB 1 KRRYDRFLGFP 12

XX RESULT 10

AAB31443
ID AAB31443 standard; peptide; 30 AA.

XX AAB31443;

DT 20-APR-2001 (first entry)

DE Peptide derived from human eukaryotic Initiation Factor 4G (elf4G).

XX Binding peptide; eukaryotic Initiation Factor 4G; elf4G; elf4E;

KW cell death; cell apoptosis; anticancer; antitumor.

XX Homo sapiens.

OS WO200078803-A2.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000WO-GB002414.

XX 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

PA Proud CG, Herbert TP, Lane DP, Fahraeus R;

DR WPI; 2001-071386/08.

PT Use of eukaryotic Initiation Factor 4E (elf4E) binding agents e.g. elf4E-

PT binding peptide (elf4E-BP) derivatives as anticancer or antitumor agents

PT for inducing apoptosis in e.g. mammalian tumor cells.

XX Disclosure; Fig 4; 46pp; English.

XX The present sequence represents a peptide derived from an eukaryotic

CC Initiation Factor 4G (elf4G) protein. The specification describes elf4G

CC and elf4E binding agents, such as peptides or peptidomimetics. These

CC binding agents are used for the induction of cell death. The binding

CC peptides are used for inducing cell apoptosis. They are used in

CC pharmaceutical compositions for anticancer or antitumor treatment of

CC mammalian cells. Specifically, the peptides result in growth inhibition

CC of, or increased cytotoxicity to tumour cells

XX Sequence 30 AA;

XX Query Match 100.0%; Score 64; DB 4; Length 30;

XX Best Local Similarity 100.0%; Pred. No. 0.00025;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 KRRYDRFLGFP 12

XX DB 1 KRRYDRFLGFP 12

XX RESULT 11

XX ADR10076

XX ADR10076 standard; protein; 903 AA.

XX ADR10076;

XX 04-NOV-2004 (first entry)

XX Human protein useful for treating neurological disease Seq 3582.

XX human; oligo-capping method; diagnostic marker; gene therapy;

XX osteoporosis; neurological disease; Alzheimer's disease;

XX Parkinson's disease; dementia; short memory; cancer;

XX sense or motor function; emotional reaction; fear response; panic;

XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX tranquiliser.

XX Homo sapiens.

XX OS

PN EPI447413-A2.
XX
PD 18-AUG-2004.
XX
PE 12-FEB-2004; 2004EP-00003145.
XX
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isegai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T,
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
DR WPI; 2004-583265/57.
DR N-PSDB; ADR08120.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 3582; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteoprotective, neuroprotective, nootropic, antiparkinsonian,
CC cyostatic and tranquiliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.
XX
SQ Sequence 903 AA;
QY
Query Match 100.0%; Score 64; DB 8; Length 903;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KCRYDREFLIGF 12
Db 550 KCRYDREFLIGF 561
RESULT 12
ADD46044 ID ADD46044 standard; protein; 1395 AA.
XX
AC ADD46044;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q04637, SEQ ID NO 11719.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002MO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'ureo D, Befort K, Coatsigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q04637.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1395 AA;
QY
Query Match 100.0%; Score 64; DB 7; Length 1395;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KCRYDREFLIGF 12
Db 413 KCRYDREFLIGF 424
RESULT 13
ADO19635 ID ADO19635 standard; protein; 1396 AA.
XX
AC ADO19635;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #282.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW

KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 OS Homo sapiens.
 XX WO2004043361-A2.
 XX
 XX 27-MAY-2004.
 XX
 XX 06-NOV-2003; 2003WO-US035266.
 XX
 XX 08-NOV-2002; 2002US-0425235P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 XX Wood WT, Wu TD;
 XX
 XX WPI; 2004-420067/39.
 XX N-PSDB; ADO19634.
 XX
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 XX treating an immune related disorder such as systemic lupus erythematosus,
 XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 XX spondyloarthritis.
 XX
 XX Claim 7; SEQ ID NO 564; 1731pp; English.
 XX
 XX The invention relates to human PRO polypeptides and the polynucleotides
 XX encoding them. The polypeptides and polynucleotides are useful for
 XX treating and diagnosing immune related disorders in mammals. The immune
 XX related disorders include systemic lupus erythematosus, rheumatoid
 XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 XX haemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 XX mellitus, immune-mediated renal disease, demyelinating diseases of the
 XX central or peripheral nervous system, demyelinating polyneuropathy,
 XX Guillain-Barre syndrome and chronic inflammatory demyelinating
 XX polyneuropathy. This sequence represents a human PRO polypeptide of the
 XX invention.
 XX
 XX Sequence 1396 AA;
 XX
 XX
 XX Query Match 100.0%; Score 64; DB 8; Length 1396;
 XX Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 12; Conservative 0;
 XX
 XX
 XX 1 KKYRDEPFLGF 12
 XX |||||
 XX 413 KKYRDEPFLGF 424
 XX
 XX
 XX RESULT 14
 XX ADP54731
 XX ID ADP54731 standard; protein; 1396 AA.
 XX
 XX ADP54731;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Human PRO protein sequence SEQ ID NO:707.
 XX
 XX human; PRO; immune related disease; inflammatory immune response;
 KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
 KW antileukemic; antidiabetic; antiinflammatory; antipsoriatic;
 KW antirheumatic; antihypertensive; CNS; dermatological; gastrointestinal;
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 KW virocidic; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX

PN WO2004039956-A2.
 XX
 XX 13-MAY-2004.
 XX
 XX 28-OCT-2003; 2003WO-US034381.
 XX
 XX 29-OCT-2002; 2002US-0422472P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
 XX Wood WT, Wu TD;
 XX
 XX WPI; 2004-376182/35.
 XX N-PSDB; ADP54730.
 XX
 XX New PRO polynucleotides and polypeptides, useful in diagnosing
 XX and treating an immune related disease, e.g. systemic lupus
 XX erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
 XX stimulating an immune response.
 XX
 XX Claim 1; SEQ ID NO 707; 3009pp; English.
 XX
 XX The present invention describes an isolated PRO nucleic acid (1). Also
 XX described: (1) a vector comprising (1); (2) a host cell comprising the
 XX vector of (1); (3) a process for producing a PRO polypeptide; (4) an
 XX isolated PRO polypeptide; (5) a chimeric molecule comprising the
 XX polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
 XX antibody which specifically binds to a polypeptide of (4); (7) a
 XX composition of matter comprising a polypeptide of (4), an agonist or
 XX antagonist of the polypeptide or an antibody that binds to the
 XX polypeptide in combination with a carrier; (8) an article of manufacture
 XX comprising a container, a label on the container and a composition of
 XX matter of (7); (9) a method of treating an immune related disease in a
 XX mammal; (10) a method for determining the presence of a PRO polypeptide
 XX in a sample suspected of having the polypeptide; (11) a method of
 XX diagnosing an immune related disease or an inflammatory immune response
 XX in mammal; (12) a method of identifying a compound that inhibits or
 XX mimics the activity of or expression of a gene encoding a PRO polypeptide
 XX; and (13) a method of stimulating the immune response in a mammal. The
 XX PRO sequences have antiallergic, antianaemic, antiarthritic,
 XX antirheumatic, antidiabetic, antiinflammatory, antipsoriatic,
 XX antineumatic, antihypertensive, CNS, dermatological, gastrointestinal,
 XX haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
 XX nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 XX virocidic activities, and can be used in gene therapy. The nucleic acid
 XX (1) and the encoded polypeptides, compositions, kits and methods are
 XX useful in diagnosing and treating an immune related disease and in
 XX stimulating an immune response. The present sequence represents a human
 XX PRO protein from the present invention.
 XX
 XX Sequence 1396 AA;
 XX
 XX
 XX Query Match 100.0%; Score 64; DB 8; Length 1396;
 XX Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 XX Matches 12; Conservative 0;
 XX
 XX
 XX 1 KKYRDEPFLGF 12
 XX |||||
 XX 413 KKYRDEPFLGF 424
 XX
 XX
 XX RESULT 15
 XX AAB18792
 XX ID AAB18792 standard; protein; 1560 AA.
 XX
 XX AAB18792;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX The human ribosome recruitment protein eIF4G1.
 XX
 XX Human; ribosome recruitment protein; eIF4G1; RNA-binding protein;
 XX
 XX

KW translational gene activation; protein binding site.
 XX
 OS Homo sapiens.
 XX
 FN W0200053779-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-1999; 99WO-EP001498.
 XX
 PR 08-MAR-1999; 99US-00264512.
 XX
 PA (EURO-) EURO MOLECULAR BIOLOGY LAB.
 XX
 PI Hentze MW, De Gregorio E;
 XX
 DR WPI; 2000-638139/61.
 DR N-PSDB; AAA75835.
 XX
 PT New nucleic acid encoding an RNA with a coding region and protein binding
 PT sites in an adjacent 5' non-coding region for translational activation of
 PT genes using the ribosome recruitment protein eIF4G.
 XX
 PS Disclosure; Fig 9A-H; 140pp; English.
 XX
 CC The present sequence represents the human ribosome recruitment protein
 CC eIF4G1. The protein is used for the translational activation of genes.
 CC The eIF4G1 protein is an RNA-binding protein. The protein is also used
 CC for the translation of RNA molecules containing protein binding sites,
 CC identifying RNA-binding proteins, protein-protein interactions, or
 CC inhibitors or enhancers of the interactions, providing a cell or subject
 CC with therapeutic proteins, controlling the levels of translation of the
 CC therapeutic proteins, screening the translation and stoichiometry of
 CC multiple subunit proteins, screening proteins that interact with an RNA
 CC binding site, and identifying the RNA binding sites
 CC
 SQ Sequence 1560 AA;

Query Match 100.0%; Score 64; DB 3; Length 1560;
 Best Local Similarity 100.0%; Pred. NO. 0.015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRYDRFLGF 12
 |||||
 Db 569 KRRYDRFLGF 580

Search completed: November 29, 2005, 22:52:14
 Job time : 117.545 secs

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OM protein - protein search, using sw model
Run on: November 29, 2005, 21:58:13 ; Search time 114.545 Seconds
(without alignments)
46.030 Million cell updates/sec

Title: US-10-019-198A-2
Perfect score: 59
Sequence: 1 RVRYSRDQLDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: geneseqp1980a:.*
2: geneseqp1990a:.*
3: geneseqp2000a:.*
4: geneseqp2001a:.*
5: geneseqp2002a:.*
6: geneseqp2003a:.*
7: geneseqp2003b:.*
8: geneseqp2004a:.*
9: geneseqp2005a:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	100.0	12	4	AAB31439	Aab31439 A wheat e
2	59	100.0	12	4	AAB31447	Aab31447 Peptide d
3	59	100.0	14	4	AAB31452	Aab31452 Peptide d
4	59	100.0	16	3	AAB31102	Aab31102 Wheat ger
5	59	100.0	16	4	AAB84407	Aab84407 4E-bindin
6	59	100.0	784	8	ADT60579	Adt60579 Plant pol
7	52	88.1	792	8	ADQ37031	Adq37031 Cell prol
8	52	88.1	792	8	ADQ15701	Adq15701 Rice stre
9	49	83.1	794	7	ABM89358	Abm89358 Rice abio
10	45	76.3	16	3	AAB11103	Aab11103 A. thalia
11	45	76.3	16	3	AAB84408	Aab84408 4E-bindin
12	45	76.3	883	3	AAQ47553	Aaq47553 Arabidops
13	45	76.3	890	3	AAQ47552	Aaq47552 Arabidops
14	45	76.3	892	3	AAQ47551	Aaq47551 Arabidops
15	42	71.2	397	8	ADX66331	Adx66331 Plant ful
16	41	69.5	717	7	ADP70241	Adp70241 C. neofor
17	40	67.8	14	4	AAB31453	Aab31453 Peptide d
18	39	66.1	343	3	AAQ47583	Aaq47583 Arabidops
19	39	66.1	343	3	AAQ50817	Aaq50817 Arabidops
20	39	66.1	347	3	AAQ30623	Aaq30623 Arabidops
21	39	66.1	361	3	AAQ50816	Aaq50816 Arabidops
22	39	66.1	361	3	AAQ45482	Aaq45482 Arabidops
23	39	66.1	500	4	ABB58961	Abb58961 Drosophil
24	38	64.4	234	4	ABB63979	Abb63979 Drosophil

25	38	64.4	664	7	ADL72419	Adl72419 Arabidops
26	38	64.4	665	3	AAQ31607	Aaq31607 Arabidops
27	38	64.4	665	5	ADL23380	Adl23380 Plant acy
28	38	64.4	665	7	ADL72258	Adl72258 Arabidops
29	38	64.4	666	8	ADT56775	Adt56775 Plant pol
30	37	62.7	159	2	AAQ86958	Aaq86958 E. coli p
31	37	62.7	236	5	ABQ49991	Abq49991 Bacteria
32	37	62.7	245	8	ADS22321	Ads22321 Bacteria
33	37	62.7	404	8	ADK71735	Adk71735 A. thalia
34	37	62.7	513	6	ABU27526	Abu27526 Protein e
35	37	62.7	532	2	AAQ86957	Aaq86957 E. coli p
36	37	62.7	553	2	AAQ86956	Aaq86956 E. coli p
37	37	62.7	621	7	ADK64864	Adk64864 Disease t
38	37	62.7	799	6	ABP73078	Abp73078 Amino aci
39	37	62.7	819	6	ABM70285	Abm70285 Phototrab
40	37	62.7	822	6	ABP73077	Abp73077 Amino aci
41	37	62.7	823	2	AAW04358	Aaw04358 E. coli p
42	37	62.7	824	6	ABU49817	Abu49817 Protein e
43	37	62.7	836	2	AAQ86954	Aaq86954 E. coli p
44	37	62.7	840	6	ABU48151	Abu48151 Protein e
45	37	62.7	840	6	ABU47291	Abu47291 Protein e

ALIGNMENTS

RESULT 1
AAB31439 standard; peptide, 12 AA.
XX
XX
AC AAB31439;
DT 20-APR-2001 (first entry)
XX
DE A wheat eukaryotic Initiation Factor 4G (eIF4G) binding peptide.
XX
KW Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
KW cell death; cell apoptosis; anticancer; antitumor.
XX
OS Homo sapiens.
XX
PN WO200078803-A2.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-GB002414.
XX
PR 21-JUN-1999; 99GB-00014480.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Proud CG, Herbert TP, Lane DP, Fahrnaeus R;
XX
DR WPI; 2001-071386/08.
XX
PT Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
XX binding peptide (eIF4E-EP) derivatives as anticancer or antitumor agents
XX for inducing apoptosis in e.g. mammalian tumor cells.
XX
PS Claim 6; Page 31; 46pp; English.
XX
CC The present sequence represents a binding peptide for an eukaryotic
CC Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
CC and eIF4E binding agents, such as peptides or peptidomimetics. These
CC binding agents are used for the induction of cell death. The binding
CC peptides are used for inducing cell apoptosis. They are used in
CC pharmaceutical compositions for anticancer or antitumor treatment of
CC mammalian cells. Specifically, the peptides result in growth inhibition
XX of, or increased cytotoxicity to, tumour cells
XX
SQ Sequence 12 AA:
Query Match 100.0%; Score 59; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
| | | | | | | | | |
Db 1 RVRYSRDQLDL 12

RESULT 2

AAB31447
ID AAB31447 standard; peptide; 12 AA.

AC AAB31447;

DT 20-APR-2001 (first entry)

DE Peptide derived from wheat eukaryotic Initiation Factor 4G (eIF4G).

KW Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;

KM cell death; cell apoptosis; anticancer; antitumor.

XX Triticum sp.

XX WO200078803-A2.

XX 28-DEC-2000.

PF 21-JUN-2000; 2000WO-GB002414.

PR 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

PI Proud CG, Herbert TP, Lane DP, Fahraeus R;

XX WPI; 2001-071386/08.

PT Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
for inducing apoptosis in e.g. mammalian tumor cells.

XX Example; Fig 5; 46pp; English.

XX The present sequence represents a peptide derived from an eukaryotic
Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
and eIF4E binding agents, such as peptides or peptidomimetics. These
binding agents are used for the induction of cell death. The binding
peptides are used for inducing cell apoptosis. They are used in
pharmaceutical compositions for anticancer or antitumor treatment of
mammalian cells. Specifically, the peptides result in growth inhibition
of, or increased cytotoxicity to tumour cells

XX Sequence 12 AA;

Query Match 100.0%; Score 59; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
| | | | | | | | | |
Db 1 RVRYSRDQLDL 12

RESULT 3

AAB31452
ID AAB31452 standard; peptide; 14 AA.

AC AAB31452;

DT 20-APR-2001 (first entry)

DE Peptide derived from wheat eukaryotic Initiation Factor 4G (eIF4G).

KW Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;

KM cell death; cell apoptosis; anticancer; antitumor.

XX Triticum sp.

XX WO200078803-A2.

XX 28-DEC-2000.

PF 21-JUN-2000; 2000WO-GB002414.

PR 21-JUN-1999; 99GB-00014480.

XX (UYDU-) UNIV DUNDEE.

PI Proud CG, Herbert TP, Lane DP, Fahraeus R;

XX WPI; 2001-071386/08.

PT Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
for inducing apoptosis in e.g. mammalian tumor cells.

XX Example; Fig 6; 46pp; English.

XX The present sequence represents a peptide derived from an eukaryotic
Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G
and eIF4E binding agents, such as peptides or peptidomimetics. These
binding agents are used for the induction of cell death. The binding
peptides are used for inducing cell apoptosis. They are used in
pharmaceutical compositions for anticancer or antitumor treatment of
mammalian cells. Specifically, the peptides result in growth inhibition
of, or increased cytotoxicity to tumour cells. note: the peptide is
biotinylated and linked to penetratin

XX Sequence 14 AA;

Query Match 100.0%; Score 59; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
| | | | | | | | | |
Db 1 RVRYSRDQLDL 12

RESULT 4

AAB11102
ID AAB11102 standard; peptide; 16 AA.

XX AAB11102;

DT 06-AUG-2003 (revised)

DT 16-FEB-2001 (first entry)

XX

DE Wheat germ eIF-4E recognition motif peptide p82.

KW Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;

KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;

XX drug; anti-obesity; anti-fat deposition; anti-metabolic.

XX Triticum aestivum.

XX WO200060932-A1.

XX 19-OCT-2000.

PF 07-APR-2000; 2000WO-CA000388.

PR 09-APR-1999; 99US-0128559P.

PR 02-FEB-2000; 2000US-0179743P.

XX (UYMC-) UNIV MCGILL.

```

XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
XX
XX WPI; 2000-672657/65.
XX
XX Non-human transgenic animal useful as model for studying lipid and
XX glucose metabolism, has germ and somatic cells containing knockout
XX mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
XX 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (I) whose
XX germ cells and somatic cells contain a knockout mutation in DNA encoding
XX a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
XX protein 1) shows a phenotype of an altered glucose and/or fat metabolism
XX when compared to a control animal. The products of the invention have
XX antidiabetic and anorectic activity. The non-human transgenic animals are
XX useful as models for the investigation of lipid and glucose metabolism,
XX energy homeostasis and associated diseases. The transgenic animals are
XX also useful for selection and identification of modulators of the
XX expression and/or activity of 4E-BP1 and for screening drugs to isolate
XX therapeutic agents which are useful as anti-obesity, anti-fat deposition
XX disorder, anti-diabetes and anti-metabolic diseases associated with fat
XX deposition disorders. The effect of the disruption of 4E-BP1 in the
XX knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
XX tissue growth, glucose metabolism and weight gain in an animal. (Updated
XX on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 16 AA;
XX
XX Query Match 100.0%; Score 59; DB 3; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 0.00058;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 RRVYGRDQLDL 12
XX |||||||||
XX 1 RRVYGRDQLDL 12
XX
XX RESULT 5
XX AAB84407
XX ID AAB84407 standard; peptide; 16 AA.
XX
XX AC AAB84407;
XX
XX DT 22-AUG-2001 (first entry)
XX
XX 4E-binding site of a p82 protein.
XX
XX 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;
XX cap-dependent translation initiation repressor; apoptosis;
XX translation initiation factor; eIF4E; Ras; cancer.
XX
XX Triflicum sp.
XX
XX WO200140293-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-CM001465.
XX
XX 02-DEC-1999; 99US-0168398P.
XX
XX (UYMC-) UNIV MCGILL.
XX PA (MINU ) UNIV MINNESOTA.
XX
XX Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;
XX
XX WPI; 2001-381379/40.
XX
XX Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,
XX useful for treating cancer or highly proliferative cells, comprises

```

Query Match	100.0%; Score 59; DB 4; Length 16;
Best Local Similarity	100.0%; Pred. No. 0.00058;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RRVYSRDQLDL 12
Db	1 RRVYSRDQLDL 12
RESULT 6	
ADT60579	
ID	ADT60579 standard; protein; 784 AA.
XX	
AC	ADT60579;
XX	
DT	13-JAN-2005 (first entry)
XX	
DE	Plant polypeptide, SEQ ID 10656.
XX	
KM	Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW	disease resistance; galactomannan production; plant growth regulator;
KW	heat tolerance; herbicide tolerance; lignin production;
KM	extreme osmotic condition tolerance; pathogens resistance;
KW	pest resistance; yield improvement; seed oil yield; seed protein yield.
XX	
OS	Viridiplantae.
XX	
PN	US2004216190-A1.
XX	
PD	28-OCT-2004.
XX	
PF	18-DEC-2003; 2003US-00739930.
XX	
PR	28-APR-2003; 2003US-00424599.
XX	
PR	28-APR-2003; 2003US-00425115.
XX	
PA	(KOVA/) KOVALIC D K.
XX	
PI	Kovalic DK;
XX	
DR	WPI; 2004-757369/74.
XX	
PT	New recombinant DNA constructs useful in the field of biochemistry and
XX	genetics, and in particular for producing transgenic plants with improved
PT	biological characteristics.
XX	
PS	Claim 2; SEQ ID NO 10656; 14pp; English.
XX	
CC	The invention relates a recombinant DNA construct comprising a
CC	polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC	1-5544) and encoding a polypeptide with any of 5544 amino acid sequences

(SEQ ID NO: 5545-11088) . The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20040216190.

CC XX Sequence 784 AA;

Query Match 100.0%; Score 59; DB 8; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
|||:|||||:
Db 63 RVRYSRDQLDL 74

RESULT 7
ADQ37031
ID ADQ37031 standard; protein; 792 AA.

XX AC ADQ37031;

XX DT 07-OCT-2004 (first entry)

XX DE Cell proliferation-related polypeptide #93.

XX KM cell proliferation related polypeptide; cell proliferation; senescence;
XX KM differentiation; stress response.

XX OS Oryza sativa.

XX PN WO2004061122-A2.

XX PD 22-JUL-2004.

XX PF 23-DEC-2003; 2003WO-US041200.

XX PR 26-DEC-2002; 2002US-0436565P.

XX RA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Cooper B;

XX

DR WPI; 2004-534388/51.

XX PT New nucleic acid molecule encoding a cell proliferation-related
PT polypeptide, useful for modulating cell proliferation, senescence,
PT differentiation, development, and stress response in plants, and for
PT producing enhanced food crops.

XX PS Claim 28; SEQ ID NO 190; 408bp; English.

CC XX The present invention relates to an isolated nucleic acid molecule
CC encoding a cell proliferation-related polypeptide. The nucleic acid
CC molecule and the encoded polypeptide, and methods are useful for
CC modulating cell proliferation, senescence, differentiation, development,
CC and stress response in plants, and for producing enhanced food crops. The
CC present sequence represents a cell proliferation-related polypeptide. The
CC present sequence is published separately from the main body of the
CC specification as EPO data.

XX SQ Sequence 792 AA;

Query Match 88.1%; Score 52; DB 8; Length 792;
Best Local Similarity 83.3%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
|||:|||||:
Db 61 RVRYSRDQLDL 72

RESULT 8
ADQ15701
ID ADQ15701 standard; protein; 792 AA.

XX AC ADQ15701;

XX DT 07-OCT-2004 (first entry)

XX DE Rice stress-related protein #55.

XX KM rice; stress-related protein; plant maturation; plant development;
KM plant proliferation; plant senescence; plant disease resistance;
KM plant stress response; transgenic plant; pest tolerance;
KM herbicide tolerance; biotic stress tolerance; abiotic stress tolerance;
KM improved nutritional value; increased yield; increased proliferation.

XX OS Oryza sativa.

XX PN WO2004061080-A2.

XX PD 22-JUL-2004.

XX PF 23-DEC-2003; 2003WO-US041098.

XX PR 26-DEC-2002; 2002US-0436564P.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Cooper B;

XX DR WPI; 2004-534374/51.

XX DR N-PSDB; ADQ15700.

XX PT New isolated nucleic acids and proteins, useful for producing transgenic
PT plants having improved properties, e.g. tolerance to pests, herbicides,
PT or biotic or abiotic stresses, improved nutritional value, or increased
PT yield or proliferation.

XX PS Claim 28; SEQ ID NO 110; 551bp; English.

CC XX The invention comprises the amino acid and coding sequences of rice
CC stress-related proteins. The DNA and protein sequences of the invention
CC are useful for regulating and controlling plant maturation and
CC development, including proliferation, senescence, disease-resistance, or

CC stress response. They are also useful for producing transgenic plants
CC having improved properties, e.g. tolerance to pests, herbicides, or
CC biotic or abiotic stresses, improved nutritional value, increased yield
CC or proliferation, or improved structure causing less loss from lodging or
CC shattering. The present amino acid sequence represents a rice stress-
CC related protein of the invention.

XX
SQ Sequence 792 AA;

Query Match 88.1%; Score 52; DB 8; Length 792;
Best Local Similarity 83.3%; Pred. No. 0.84;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRVYSRDQLDL 12
|||:||||:|
Db 61 RRVYTRDQLLEL 72

RESULT 9
ABM89358
ID ABM89358 standard; protein; 794 AA.

XX ABM89358;
XX
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polypeptide SEQ ID NO:7604.
XX
XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

XX Oryza sativa.

XX WO2003008540-A2.

XX 30-JAN-2003.

XX 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.

XX 24-SEP-2001; 2001US-0314662P.

XX 26-SEP-2001; 2001US-0325277P.

XX 21-NOV-2001; 2001US-0332132P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
XX Moughamer T, Froyart N, Ritke D, Zhu T;

XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.

XX Claim 1; SEQ ID NO 7604; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX cells, and plants containing such polynucleotides. Also disclosed are
XX methods for using the polynucleotides and polypeptides to alter the
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX agriculture. The nucleic acid is useful for determining whether a test
XX plant has been exposed to an abiotic stress condition. It is also useful
XX for selecting an agent that alters abiotic stress regulated
XX polynucleotide expression in a plant cell, and to identify a homolog or
XX ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
XX molecule and the polypeptide encoded by it are useful in altering the
XX responsiveness of a plant to an abiotic stress, such as cold stress, salt
XX stress, osmotic stress or any of their combinations. The present sequence
XX is used in the exemplification of the invention

XX Sequence 794 AA;

Query Match 83.1%; Score 49; DB 7; Length 794;
Best Local Similarity 75.0%; Pred. No. 3.1;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRVYSRDQLDL 12
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Db 64 RRVYTRDQLVEL 75

RESULT 10
AAB1103
ID AAB1103 standard; peptide; 16 AA.

XX AAB1103;
XX
XX 16-FEB-2001 (first entry)
XX
XX A. thaliana eif-4E recognition motif peptide eif4G.

XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
XX knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
XX drug; anti-obesity; anti-fat deposition; anti-metabolic.

XX Arabidopsis thaliana.

XX WO200060932-A1.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-CA000388.

XX 09-APR-1999; 99US-0128559P.

XX 02-FEB-2000; 2000US-0179743P.

XX (UWMC-) UNIV MCGILL.

XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;

XX WPI; 2000-672657/65.

XX Non-human transgenic animal useful as model for studying lipid and
XX glucose metabolism, has germ and somatic cells containing knockout
XX mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
XX 1.

XX Disclosure; Fig 7; 80pp; English.

XX This invention describes a novel non-human transgenic animal (I) whose
XX germ cells and somatic cells contain a knockout mutation in DNA encoding
XX a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
XX protein 1) shows a phenotype of an altered glucose and/or fat metabolism
XX when compared to a control animal. The products of the invention have
XX antidiabetic and anorectic activity. The non-human transgenic animals are
XX useful as models for the investigation of lipid and glucose metabolism,
XX energy homeostasis and associated diseases. The transgenic animals are
XX also useful for selection and identification of modulators of the
XX expression and/or activity of 4E-BP1 and for screening drugs to isolate
XX therapeutic agents which are useful as anti-obesity, anti-fat deposition
XX disorder, anti-diabetes and anti-metabolic diseases associated with fat
XX deposition disorders. The effect of the disruption of 4E-BP1 in the
XX knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
XX tissue growth, glucose metabolism and weight gain in an animal

XX Sequence 16 AA;

Query Match 76.3%; Score 45; DB 3; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRVYSRDQLDL 12
|||:||||:|
Db 1 RRVYTRDQLLEL 12

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RESULT 11
AAB84408
ID AAB84408 standard; peptide; 16 AA.
XX
AC AAB84408;
XX
DT 22-AUG-2001 (first entry)
XX
DE 4E-binding site of a elf4G protein.
XX
KW 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;
KW cap-dependent translation initiation repressor; apoptosis;
KW translation initiation factor; elf4E; Ras; cancer.
XX
OS Arabidopsis thaliana.
XX
PN W0200140293-A2.
XX
PD 07-JUN-2001.
XX
PE 01-DEC-2000; 2000WO-CN001465.
XX
PR 02-DEC-1999; 99US-0168398P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;
XX
DR WPI; 2001-381379/40.
XX
PT Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,
PT useful for treating cancer or highly proliferative cells, comprises
PT decreasing the amount of elf4F pre-initiation complex, relieving an
PT apoptosis block.
XX
PS Disclosure; Fig 6; 80pp; English.
XX
CC AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is
CC a repressor of cap-dependent translation initiation, and selectively
CC activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-
CC induced chemoresistance. The effects of 4E-BP1 are strictly dependent on
CC its ability to sequester the translation initiation factor elf4E, thereby
CC preventing its assembly into an active pre-initiation complex. The
CC specification describes a method for inducing apoptosis in a cell in
CC which the apoptosis pathway is inhibited. The method comprises decreasing
CC the amount of elf4F pre-initiation complex by sequestration of elf4E,
CC thus relieving an apoptosis block. The method is useful for modulating
CC pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-
CC transformed cells. Thus, the method is particularly useful for treating
CC cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion
CC is useful for treating high proliferative cells
XX
XX
SQ Sequence 16 AA;
Query Match 76.3%; Score 45; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVRRYSRDDLDL 12
||:|:|:|:|:|
Db 1 RVKYYRQQLLEL 12
RESULT 12
AAG47553
ID AAG47553 standard; protein; 883 AA.
XX
AC AAG47553;
XX
DT 18-OCT-2000 (first entry)
XX
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 59949.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
FD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PF 25-FEB-1999; 99US-0121825P.
XX
PR 05-MAR-1999; 99US-0123180P.
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PR 09-MAR-1999; 99US-0123548P.
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PR 23-MAR-1999; 99US-0125788P.
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PR 25-MAR-1999; 99US-0126264P.
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PR 29-MAR-1999; 99US-0126785P.
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PR 06-APR-1999; 99US-0128234P.
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PR 21-JUN-1999; 99US-0139817P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 76.3%; Score 45; DB 3; Length 883;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYRGDQDL 12
DB 176 RYKTYREQLLEL 187

RESULT 13
AA647552
ID AA647552 standard; protein; 890 AA.
XX AA647552;
AC
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59948.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.

PR 13-JUL-1999; 99US-0143542P.
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PR 24-SEP-1999; 99US-0155659P.
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PR 29-SEP-1999; 99US-0156596P.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 76.3%; Score 45; DB 3; Length 892;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKYSRDQLDL 12
Db 185 RVKYTEQLLEL 196

RESULT 15
ADK66331
ID ADK66331 standard; protein; 397 AA.

XX ADK66331;

DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 37174.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
protein content.

XX Unidentified.

OS US2004034888-A1.

PN 19-FEB-2004.

PD 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU//) LIU J.
 PA (ZHOU//) ZHOU Y.
 PA (KOVA//) KOVALIC D K.
 PA (SCRE//) SCREEN S E.
 PA (TABSA//) TABASKA J E.
 PA (CAOY//) CAO Y.

XX Llu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

PS Claim 1; SEQ ID NO 37174; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 397 AA;

Query Match 71.2%; Score 42; DB 8; Length 397;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVYGRDQLDL 12
 ||:|||||:
 Db 363 RLKTSRDELAL 374

Search completed: November 29, 2005, 22:52:17
 Job time : 117.545 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 29, 2005, 22:35:24 ; Search time 18.8182 Seconds
(without alignments)
61.356 Million cell updates/sec

Title: US-10-019-198a-2
Perfect score: 59
Sequence: 1 RVRYSRDQLDL 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	100.0	787	2	A44452	translactation initia
2	40	67.8	302	2	S36188	beta-lactamase (EC
3	39	66.1	312	2	F82883	glycosyltransferas
4	39	66.1	347	2	H84608	probable RNA-bindi
5	39	66.1	843	2	T22182	hypothetical prote
6	38	64.4	231	2	H83932	two-component resp
7	38	64.4	613	2	B96501	hypothetical prote
8	38	64.4	665	2	G96530	probable acyl CoA
9	38	64.4	666	2	T07928	probable long-chain
10	38	64.4	689	2	T09007	ABC-transporter ho
11	37	62.7	158	2	C87354	hypothetical prote
12	37	62.7	236	2	AE1187	two-component resp
13	37	62.7	236	2	AG1762	two-component resp
14	37	62.7	301	2	T21803	hypothetical prote
15	37	62.7	524	2	D82265	GDBR family prote
16	37	62.7	621	2	S70121	signal recognition
17	37	62.7	824	2	AC0412	penicillin-binding
18	37	62.7	840	2	AG0526	penicillin-binding
19	37	62.7	844	1	ZPECPB	penicillin-binding
20	37	62.7	844	2	A85499	peptidoglycan synt
21	37	62.7	844	2	A99648	peptidoglycan synt
22	37	62.7	1310	1	TS3587	proline dehydrogen
23	37	62.7	1320	1	S66279	proline dehydrogen
24	37	62.7	1320	2	AE0633	proline dehydrogen
25	36	61.0	143	2	G71980	hypothetical prote
26	36	61.0	299	2	S60971	probable membrane
27	36	61.0	361	2	H83412	molybdenum transpo
28	36	61.0	747	2	A84632	probable eukaryoti
29	36	61.0	885	2	G83260	antipeptidase N P

30	36	61.0	923	2	B83574	hypothetical prote
31	35	59.3	60	2	S09227	homeotic protein H
32	35	59.3	126	2	H75433	hypothetical prote
33	35	59.3	179	2	G75603	hypothetical prote
34	35	59.3	204	2	G95276	probable transcrip
35	35	59.3	254	2	B87396	DNA-binding respon
36	35	59.3	270	2	JN0767	homeobox protein H
37	35	59.3	311	2	A69095	cobalt transport A
38	35	59.3	328	2	B84263	succinoglycan bios
39	35	59.3	335	2	T04029	hypothetical prote
40	35	59.3	335	2	A86464	hypothetical prote
41	35	59.3	364	2	T08903	hypothetical prote
42	35	59.3	428	2	F71209	probable phosphogl
43	35	59.3	448	2	C81718	signal recognition
44	35	59.3	509	2	A57512	beta-glucosidase B
45	35	59.3	684	2	T40319	hypothetical prote

ALIGNMENTS

RESULT 1

A44452
translactation initiation factor eif-4f isozyme form subunit p82 - wheat
C/Species: Triticum sp. (wheat)
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44452
R/Allen, M.L.; Metz, A.M.; Timmer, R.T.; Rhoads, R.E.; Browning, K.S.
J. Biol. Chem. 267, 2332-2336, 1992
A/Title: Isolation and sequence of the cDNAs encoding the subunits of the isozyme form c
A/Reference number: A44452; MUID:93054655; PMID:1385417
A/Accession: A44452
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-787 <Alt>
A/Cross-references: UNIPROT:003387; UNIPARC:UP1000017A01D
A/Note: sequence extracted from NCBI backbone (NCBIP:118288)

Query Match 100.0%; Score 59; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
DB 62 RVRYSRDQLDL 73

RESULT 2

S36188
beta-lactamase (EC 3.5.2.6) I precursor - Streptomyces lactamdurans
C/Species: Streptomyces lactamdurans
C/Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
C/Accession: S36188; S22750
R/Coque, J.-J. R.; Liras, P.; Martin, J.F.
EMBO J. 12, 631-639, 1993
A/Title: Genes for a beta-lactamase, a penicillin-binding protein and a transmembrane p
A/Reference number: S36188; MUID:93178438; PMID:8440253
A/Accession: S36188
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-302 <COO>
A/Cross-references: UNIPROT:Q06316; UNIPARC:UP100001269D1; EMBL:Z13971; NID:944996; P
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
C/Genetics:
A/Gene: bla
A/Start codon: GNG
C/Superfamily: Beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase; penicillin resistance
F/1-29/Domain: signal sequence #status predicted <Sig>
F/30-302/Product: beta-lactamase I #status predicted <Mat>
F/85/Active site: Ser #status predicted

Query Match 67.8%; Score 40; DB 2; Length 302;

Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VRYSRDQLDL 11
Db 108 VRYSKDELL 117

RESULT 3

F82883
glycosyltransferase U503 [imported] - Ureaplasma urealyticum
C/Species: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: F82883

R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000

A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mit
A/Reference number: A82870

A/Accession: F82883

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-312 <GLA>

A/Cross-references: UNIPARC:UPI00000C1C98; GB:AE002148; GB:AF22894; NID:96899495; PIDN:

A/Experimental source: serovar 3; biovar 1

C/Genetics:

A/Gene: epsg; U503

A/Genetic code: SGC3

Query Match 66.1%; Score 39; DB 2; Length 312;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VRYSRDQLDL 12
Db 217 IRFSNDLDDL 227

RESULT 4

H84608
probable RNA-binding protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: H84608

R/Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;
euse, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: H84608

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-347 <STO>

A/Cross-references: UNIPROT:Q9SHZ6; UNIPARC:UPI000017A786; GB:AE002093; NID:94587587; PT

C/Genetics:

A/Gene: At2g22090

A/Map position: 2

Query Match 66.1%; Score 39; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YSRDQLDL 12
Db 70 YSKDQLVLDL 78

RESULT 5

T22182
hypothetical protein F44F1.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22182; T23650

R/Dobson, R.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19527

A/Accession: T22182

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-843 <WIL>

A/Cross-references: UNIPROT:O02264; UNIPARC:UPI00000751A6; EMBL:Z81083; PIDN:CAB03105.1;

A/Experimental source: clone F44F1

R/Dobson, R.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z19777

A/Accession: T23650

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-843 <WIL>

A/Cross-references: UNIPARC:UPI00000751A6; EMBL:Z93385; PIDN:CAB07642.1; GSPDB:GN00019; C

A/Experimental source: clone MOIES

C/Genetics:

A/Gene: CESP:F44F1.7

A/Map position: 1

A/Introns: 98/1; 375/1; 487/1; 657/3

Query Match 66.1%; Score 39; DB 2; Length 843;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVYSRDQLDL 12
Db 284 RLKSEDDQLDL 295

RESULT 6

H83932
two-component response regulator BH2264 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: H83932

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: H83932

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-231 <STO>

A/Cross-references: UNIPROT:Q9KAM3; UNIPARC:UPI00000C3B63; GB:AP001514; GB:BA000004; NID:

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH2264

C/Superfamily: ompR protein; response regulator homology

Query Match 64.4%; Score 38; DB 2; Length 231;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YSRDQLDL 12
Db 171 YTRQQLDL 179

RESULT 7

B96501
hypothetical protein F236.12 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B96501

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luores, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96501
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-613 <STO>
 A:Cross-references: UNIPROT:Q9MA69; UNIPARC:UPI00000AAZBC; GB:AE005173; NID:G7523688; PI
 C:Genetics:
 A:Gene: F206.12
 A:Map position: 1

Query Match 64.4%; Score 38; DB 2; Length 613;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
 |:::|
 Db 184 RQNFSDQLDL 195

RESULT 8
 G96530
 probable acyl CoA synthetase [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: G96530
 R:Thellogis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96530
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-665 <STO>
 A:Cross-references: UNIPROT:Q9XIA9; UNIPARC:UPI00000BD72; GB:AE005173; NID:G5430757; PI
 C:Genetics:
 A:Gene: F13F21.14
 A:Map position: 1
 C:Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology

Query Match 64.4%; Score 38; DB 2; Length 665;
 Best Local Similarity 58.3%; Pred. No. 47;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
 |:::|
 Db 29 RCKYAKDGLDL 40

RESULT 9
 T07928
 probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) isoform 1 - *rape*
 N:Alternate names: acyl CoA synthetase
 C:Species: *Brassica napus* (rape)
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C:Accession: T07928
 R:Fulla, M.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z16223
 A:Accession: T07928
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-666 <FUL>

A:Cross-references: UNIPROT:Q96537; UNIPARC:UPI00000ACC47; EMBL:Z72153; PIDN:CAA96523.1
 A:Experimental source: cv. Aeceri; 20-26 days after flowering; developing pods
 C:Function:
 A:Description: activates long chain fatty acids
 C:Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology
 C:Keywords: acid-thiol ligase; coenzyme A
 F:100-646/Domain: acetate-CoA ligase homology <ACL>

Query Match 64.4%; Score 38; DB 2; Length 666;
 Best Local Similarity 58.3%; Pred. No. 47;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RVRYSRDQLDL 12
 |:::|
 Db 29 RCKYAKDGLDL 40

RESULT 10
 T09007
 ABC-transporter homolog Scnt - *Streptococcus pyogenes*
 C:Species: *Streptococcus pyogenes*
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T09007
 R:Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
 Appl. Environ. Microbiol. 59, 1969-1971, 1993
 A:Title: Cloning of the gene encoding streptococcal A-PF22, a novel lantibiotic produced
 A:Reference number: A58598; MUID:93319301; PMID:8328813
 A:Accession: T09007
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-689 <HYN>
 A:Cross-references: UNIPROT:Q31053; UNIPARC:UPI00000AF8A4; EMBL:AF026542; NID:G2502065;
 A:Experimental source: strain PF22
 C:Genetics:
 A:Gene: scnt
 C:Superfamily: membrane associated MDR-type ABC transporter CAC2755; ATP-binding cassette

Query Match 64.4%; Score 38; DB 2; Length 689;
 Best Local Similarity 60.0%; Pred. No. 49;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVRYSRDQL 10
 |:::|
 Db 110 RIKYSRDEFL 119

RESULT 11
 C87354
 hypothetical protein C00846 [imported] - *Caulobacter crescentus*
 C:Species: *Caulobacter crescentus*
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: C87354
 R:Nietman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolich,
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: C87354
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-158 <STO>
 A:Cross-references: UNIPROT:Q9A9W5; UNIPARC:UPI00000C71B9; GB:AE005673; NID:G13422101; P
 C:Genetics:
 A:Gene: C00846

Query Match 62.7%; Score 37; DB 2; Length 158;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RYSRDQLDL 12
 |:::|
 Db 84 RMSRDLIDL 93

RESULT 12

AE1387

two-component response phosphate regulator phop [imported] - *Listeria monocytogenes* (str C)
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AE1387

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AE1387

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-236 <GLA>
A:Cross-references: UNIPROT:Q8Y4E5; UNIPARC:UPI00000CF21A; GB:NC_003210; PIDN:CAD00579.1

A:Experimental source: strain EGD-e
C:Genetics:

A:Gene: phop
C:Superfamily: ompR protein; response regulator homology

Query Match 62.7%; Score 37; DB 2; Length 236;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSRDQLD 11
:|||||

Db 180 FSRDQLD 187

RESULT 13

AG1762

two-component response phosphate regulator phop [imported] - *Listeria innocua* (strain C)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG1762

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1762

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-236 <GLA>
A:Cross-references: UNIPROT:Q937Z2; UNIPARC:UPI00000CC931; GB:AL592022; PIDN:CAC97871.1;

A:Experimental source: strain Clp11262
C:Genetics:

A:Gene: phop
C:Superfamily: ompR protein; response regulator homology

Query Match 62.7%; Score 37; DB 2; Length 236;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSRDQLD 11
:|||||

Db 180 FSRDQLD 187

RESULT 14

T21803

hypothetical protein F35G12.10 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21803

R:Chui, C.

submitted to the EMBL Data Library, October 1994
A:Reference number: Z19473

A:Accession: T21803

A:Status: preliminary; translated from GB/EMBL/DDB
A:Molecule type: DNA

A:Residues: 1-301 <NTL>
A:Cross-references: UNIPROT:Q20053; UNIPARC:UPI00000776D1; EMBL:Z46242; PIDN:CAA86329.1;

A:Experimental source: clone F35G12

C:Genetics:
A:Gene: CSP: F35G12.10

A:Map position: 3
A:Introns: 26/1; 48/1; 169/1; 235/2

Query Match 62.7%; Score 37; DB 2; Length 301;
Best Local Similarity 58.3%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RVRYSRDQLD 12
:|||||

Db 259 KAFERDQLKL 270

RESULT 15

D82265

GGDEF family protein VC0900 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: D82265

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P. L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: D82265

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1524 <HEI>
A:Cross-references: UNIPROT:Q9KTK2; UNIPARC:UPI00000C2E01; GB:AE004174; GB:AE003852; NID:

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:

A:Gene: VC0900
A:Map position: 1

Query Match 62.7%; Score 37; DB 2; Length 524;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQL 9
:|||||

Db 335 RMYSKDDM 343

Search completed: November 29, 2005, 23:02:32
Job time : 20.8182 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2005, 22:35:04 ; Search time 115.091 Seconds
(without alignments)
73.562 Million cell updates/sec

Title: US-10-019-198A-2
Perfect score: 59
Sequence: 1 RVRYSRDQLDL 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	787	2	Q41583_WHEAT
2	59	100.0	788	1	IP41_WHEAT
3	52	88.1	792	2	Q84PB3_ORYSA
4	52	88.1	923	2	Q7XRB9_ORYSA
5	49	83.1	780	2	Q6K641_ORYSA
6	45	76.3	751	2	Q9FUM7_ARYTH
7	45	76.3	776	2	Q8H0T8_ARYTH
8	45	76.3	780	2	Q8H179_ARYTH
9	45	76.3	780	2	Q93ZT6_ARYTH
10	44	74.6	108	2	Q4P4H6_USTMA
11	43	72.9	587	2	Q5DB11_SCHUA
12	43	72.9	711	2	Q5Z5O3_ORYSA
13	43	72.9	1524	2	Q5A2Q2_EMENT
14	41	69.5	60	2	Q4VMT9_GURUC
15	41	69.5	232	2	Q8Y1Y7_RALSO
16	41	69.5	307	2	Q4HV16_GIBZE
17	41	69.5	309	2	Q675T8_GURUC
18	41	69.5	724	2	Q9HF03_CRYNE
19	41	69.5	726	2	Q55Z33_CRYNE
20	41	69.5	726	2	Q5XNE9_CRYNE
21	40	67.8	302	1	BLAC_NOCIA
22	40	67.8	352	2	Q5B8R7_EMENT
23	40	67.8	356	2	P79037_EMENT
24	40	67.8	644	2	Q7MX48_PORCI
25	39	66.1	96	2	Q53116_MYCLE
26	39	66.1	208	2	Q9XYT5_9CNID
27	39	66.1	213	2	Q46126_HELTR
28	39	66.1	312	2	Q9PEY7_UREPA
29	39	66.1	343	2	Q8L990_ARYTH
30	39	66.1	343	2	Q9SHZ6_ARYTH
31	39	66.1	344	2	Q8RYD4_ARYTH

32	39	66.1	443	2	Q8MZV2_HALMA	Q8mzv2 halotis wa
33	39	66.1	496	2	Q5XJ11_BRARE	Q5xj11 brachydanio
34	39	66.1	500	2	Q8SYH2_DROME	Q8syh2 drosophila
35	39	66.1	500	2	Q9W373_DROME	Q9w373 drosophila
36	39	66.1	657	2	Q4LNL8_9BURK	Q4lnl8 burkholderi
37	39	66.1	843	2	Q02264_CAEEL	Q02264 caenorhabdi
38	39	66.1	1009	2	Q4PBB1_USTMA	Q4pbb1 ustilago ma
39	39	66.1	1747	2	Q7QV95_GITALA	Q7qv95 giardia lam
40	38	64.4	148	2	Q4LUC9_9BURK	Q4luc9 burkholderi
41	38	64.4	175	2	Q892Y1_CLOTE	Q892y1 cioscridium
42	38	64.4	185	2	Q4Y905_PLACH	Q4y905 plasmodium
43	38	64.4	194	2	Q9RA50_THERM	Q9ra50 thermus the
44	38	64.4	231	2	Q9KAM3_BACCH	Q9kam3 bacillus ha
45	38	64.4	234	2	Q9VX62_DROME	Q9vx62 drosophila

ALIGNMENTS

RESULT 1					
ID	Q41583_WHEAT	Q41583_WHEAT PRELIMINARY;	PRT;	787 AA.	
AC	Q41583;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Initiation factor (Iso)4F p82 subunit.				
OS	Triticum aestivum (Wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticaceae; Triticum.				
OX	NCBI_TaxID=4565;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Growing sprout tips;				
RX	MEDLINE=93054655; PubMed=1385417;				
RA	Allen M.L., Metz A.M., Timmer R.T., Rhoads R.E., Browning K.S.;				
RT	"Isolation and sequence of the cDNAs encoding the subunits of the				
RT	RT isozyme form of wheat protein synthesis initiation factor 4F."				
RL	J. Biol. Chem. 267:23232-23236(1992).				
DR	EMBL; M95746; AAA74724.1; -; mRNA.				
DR	HSSP; Q43432; 1HU3.				
DR	GO; GO:0003723; P:RNA binding; IEA.				
DR	GO; GO:0003743; F:translation initiation factor activity; IEA.				
DR	InterPro; IPR003890; IF_eIF4G.				
DR	InterPro; IPR003891; IF_eIF4G_MA3.				
DR	Pfam; PF02847; MA3; 1.				
DR	Pfam; PF02844; MIF4G; 1.				
DR	SMART; SM00544; MA3; 1.				
KW	SMART; SM00543; MIF4G; 1.				
SQ	SEQUENCE 787 AA; 86579 MW; C3FA312F17E8AF73 CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 59; DB 2; Length 787;					
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 RVRYSRDQLDL 12				
DB	62 RVRYSRDQLDL 73				
RESULT 2					
ID	IP41_WHEAT	IP41_WHEAT STANDARD;	PRT;	788 AA.	
AC	Q03387;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	10-MAY-2005 (Rel. 47, Last annotation update)				
DE	Eukaryotic initiation factor (Iso)4F subunit p82-34 (eIF-4F p82-				
DE	34).				
OS	Triticum aestivum (Wheat).				

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN
  [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 193-200; 255-284;
RP 411-419; 448-458 AND 681-688.
RC TISSUE=Root tip;
RX MEDLINE=9305655; PubMed=1385417;
RA Allen M.L., Metz A.M., Timmer R.T., Rhoads R.E., Browning K.S.;
RT "Isolation and sequence of the cDNAs encoding the subunits of the
RT isozygic form of wheat protein synthesis initiation factor 4F.";
RL J. Biol. Chem. 267:23232-23236(1992).
RN
  [2]
RP SEQUENCE REVISION.
RA Metz A.M.;
RA Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC
  -1- FUNCTION: Functions in close association with EIF4B and EIF4A in
  CC ATP-dependent RNA-unwinding.
  CC -1- MISCELLANEOUS: In higher plants two isoforms of EIF4F have been
  CC identified, named isoform EIF4F and isoform EIF(ISO)4F. Isoform
  CC EIF4F has subunits p220 and p28, whereas isoform EIF(ISO)4F has
  CC subunits p82 and p26. Two forms of p82 have been identified, p82-
  CC 34 and p82-16.
  CC -1- SIMILARITY: Belongs to the eIF4G family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: M95747; AAA16209.1; -, mRNA.
DR PIR: A44452; A44452.
DR HSP: Q43432; IH03.
DR Gramene; Q03387; -.
DR InterPro: IPR003890; IF_eIF4G.
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 1.
DR Pfam: PF02854; MIF4G; 1.
DR SMART; SM00543; MIF4G; 1.
DR SMART; SM00543; MIF4G; 1.
KW Direct protein sequencing; Initiation factor; Protein biosynthesis;
KM RNA-binding.
SQ SEQUENCE 788 AA; 86295 MW; 476DE9EB9DEB4715 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLIDL 12
DB 63 RVRYSRDQLIDL 74

RESULT 3
084P93 ORYSA PRELIMINARY; PRT; 792 AA.
AC 084P93;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Eukaryotic initiation factor-like protein.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN
  [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22584437; PubMed=12684538; DOI=10.1073/pnas.0737574100;
RA Cooper B., Clarke M., Budworth P., Kreps J., Hutchison D., Park S.,
RA Guimil S., Dunn M., Lugjubuhl P., Ellero C., Goff S.A., Glaesbrook J.;

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RT "A network of rice genes associated with stress response and seed
RT development.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4945-4950(2003).
DR EMBL: AY224450; AA072569.1; -, mRNA.
DR HSP: Q43432; IH03.
DR Gramene; Q84P93; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR003890; IF_eIF4G.
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam; PF02847; MA3; 1.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SM00544; MIF4G; 1.
DR SMART; SM00543; MIF4G; 1.
KW Initiation factor.
SQ SEQUENCE 792 AA; 86905 MW; 37703FDB5CC2C2E73 CRC64;

Query Match 88.1%; Score 52; DB 2; Length 792;
Best Local Similarity 83.3%; Pred. No. 0.93;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLIDL 12
DB 61 RVRYSRDQLIDL 72

RESULT 4
07XT80 ORYSA PRELIMINARY; PRT; 923 AA.
AC 07XT80;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE OSUNBa029H02.9 protein.
GN Name=OSUNBa029H02.9;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN
  [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Fang Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Ren H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu W., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL: AL606594; CA601628.3; -, Genomic_DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
SQ SEQUENCE 923 AA; 102231 MW; FC90A2B43DE7058B CRC64;

Query Match 88.1%; Score 52; DB 2; Length 923;
Best Local Similarity 83.3%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLIDL 12
DB 61 RVRYSRDQLIDL 72

RESULT 5
06K641 ORYSA PRELIMINARY; PRT; 780 AA.
AC 06K641;

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```
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Purative eukaryotic Initiation factor (iso14F subunit p82-34 (EIF-
DE (iso14F p82-34)).
GN Name=O1004_A05.11;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacridae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005286; BAD19680.1; -; Genomic_DNA.
DR Cramene; O6K61; -;
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR003890; IF_eIF4G.
DR InterPro; IPR003891; IF_eIF4G_MAJ.
DR Pfam; PF02847; MAJ; 1.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SM00544; MAJ; 1.
DR SMART; SM00543; MIF4G; 1.
KW Initiation factor.
SQ SEQUENCE 780 AA; 85988 MW; 1C25ACB6B620C907 CRC64;

Query Match 83.1%; Score 49; DB 2; Length 780;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRVSRDQLDL 12
Db 64 RRVYTRDQLVEL 75

RESULT 6
O9FUM7 ARATH PRELIMINARY; PRT; 751 AA.
ID O9FUM7 ARATH PRELIMINARY; PRT; 751 AA.
AC O9FUM7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Eukaryotic Initiation factor 4, eIF4-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Physically assigned P1 and TAC clones.";
RL DNA Ref. 5:203-216 (1998).
DR EMBL; AB013396; BAB08857.1; -; Genomic_DNA.
DR HSSP; O43432; IHU3.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR003890; IF_eIF4G.
DR InterPro; IPR003891; IF_eIF4G_MAJ.
DR Pfam; PF02847; MAJ; 1.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SM00544; MAJ; 1.
DR SMART; SM00543; MIF4G; 1.
RN [1]
RP NUCLEOTIDE SEQUENCE.
SQ SEQUENCE 751 AA; 82359 MW; 771AD35200498882 CRC64;
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Query Match 76.3%; Score 45; DB 2; Length 751;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRVSRDQLDL 12
Db 69 RRVYTRDQLVEL 80

RESULT 7
O8H078 ARATH PRELIMINARY; PRT; 776 AA.
ID O8H078 ARATH PRELIMINARY; PRT; 776 AA.
AC O8H078;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Eukaryotic Initiation factor 4, eIF4-like protein.
GN Name=At5g57870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Nguyen M., Tripp M., Jones T., Wu T.,
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamaya A., Kawai J.,
RA Kim C., Itoh J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
RA Ecker J., Noelogis A., Davis R.W.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT02056; AAN72067.1; -; mRNA.
DR HSSP; O43432; IHU3.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR003890; IF_eIF4G.
DR InterPro; IPR003891; IF_eIF4G_MAJ.
DR Pfam; PF02847; MAJ; 1.
DR Pfam; PF02854; MIF4G; 1.
DR SMART; SM00544; MAJ; 1.
DR SMART; SM00543; MIF4G; 1.
KW Initiation factor.
SQ SEQUENCE 776 AA; 85171 MW; CB0500ABA0E516FF CRC64;

Query Match 76.3%; Score 45; DB 2; Length 776;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRVSRDQLDL 12
Db 69 RRVYTRDQLVEL 80

RESULT 8
O8H179 ARATH PRELIMINARY; PRT; 780 AA.
ID O8H179 ARATH PRELIMINARY; PRT; 780 AA.
AC O8H179;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Eukaryotic Initiation factor 4, eIF4-like protein.
GN Name=At5g57870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
```

RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Heuan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Tang C.C., Torouni M., Wallender E.K., Wong C.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
 RA Theologis A., Davis R.W.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Heuan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Shinn P., Tang C.C., Torouni M., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
 RA Davis R.W.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT000467; AAN17444.1; -; mRNA.
 DR EMBL; BT003424; AAC30087.1; -; mRNA.
 DR HSSP; O43432; IHU3.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR003890; IF_eIF4G.
 DR InterPro; IPR003891; IF_eIF4G_MA3.
 DR Pfam; PF02847; MA3; 1.
 DR Pfam; PF02854; MIF4G; 1.
 DR SMART; SM00544; MA3; 1.
 DR SMART; SM00543; MIF4G; 1.
 KW Initiation factor.
 SQ SEQUENCE 780 AA; 85575 MW; 654C189D869CE365 CRC64;
 Query Match 76.3%; Score 45; DB 2; Length 780;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVVRSRDQLDL 12
 Db 69 RVKXTRQLEL 80
 RESULT 9
 Q93ZT6 ARATH PRELIMINARY; PRT; 780 AA.
 ID Q93ZT6 ARATH PRELIMINARY; PRT; 780 AA.
 AC Q93ZT6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative eukaryotic initiation factor eIF4 (Putative eukaryotic
 DE Initiation factor 4).
 GN Name=At5G57870;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_Taxid=3702;
 OX NCBI_Taxid=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriomi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriomi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY056266; AAL07115.1; -; mRNA.
 DR EMBL; AY091258; AAM14197.1; -; mRNA.
 DR HSSP; O43432; IHU3.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR003890; IF_eIF4G.
 DR InterPro; IPR003891; IF_eIF4G_MA3.
 DR Pfam; PF02847; MA3; 1.
 DR Pfam; PF02854; MIF4G; 1.
 DR SMART; SM00544; MA3; 1.
 DR SMART; SM00543; MIF4G; 1.
 KW Initiation factor.
 SQ SEQUENCE 780 AA; 85571 MW; 122772237F6C6234 CRC64;
 Query Match 76.3%; Score 45; DB 2; Length 780;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVVRSRDQLDL 12
 Db 69 RVKXTRQLEL 80
 RESULT 10
 Q4PAH6 USTWA PRELIMINARY; PRT; 108 AA.
 ID Q4PAH6 USTWA PRELIMINARY; PRT; 108 AA.
 AC Q4PAH6
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=UM04987.1;
 OS Ustilago maydis 521.
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OC NCBI_Taxid=237631;
 OX NCBI_Taxid=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=521;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-Sahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Atacchi H., Amburster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitsheseyn B., Bloom T., Bye J., Boguslavsky L.,
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshtang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Dufey N., Dupes A., Ekins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gierre S.,
 RA Gutirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseis S., Karlsson E.,
 RA Kelis C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Legey J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., MacDonald J., McLean C., Major J.,
 RA Manning J., Marabella R., Marr K., Matthews C., Maucell E.,
 RA McCarthy J., McDonough S., McInnes T., Meltrin T., Meneis L.,
 RA Mesirov J., Mihalov A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhang P., Pigani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Riese C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schubach R., Seaman C., Settupalli S., Sharpe T.,

RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Staiker J., Stange-Thomann N., Stavropoulos S.,
 RA Steenson K., Stone C., Stone S., Stubbs M., Talamaa J., Tchinga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Teemia T., Tromo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wymann D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.,
 RT "The genome sequence of *Ustilago maydis*,"
 RL submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL: ACP0100184; EAK85760.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 108 AA; 11407 MW; E61B76DB8C16E7A CRC64;

Query Match 74.6%; Score 44; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 3.5;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RVYRSRDQLDL 12
 DB 34 RYSYRDLNL 45

RESULT 11
 Q5D811.SCHJA PRELIMINARY; PRT; 587 AA.
 AC Q5D811;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Schistosoma japonicum (blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 CC Schistosomatidae; Schistosomatidae; Schistosoma.
 RX NCBI_TaxID=6182;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Han Z.,
 RT Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY816143; AAM27875.1; -; mRNA.
 DR EMBL: AY816143; AAM27875.1; -; mRNA.
 DR InterPro; IPR003890; IPR003890; IPR003890; IPR003890;
 DR Pfam; PF02854; MIF4G; 1.
 DR SMART; SM00543; MIF4G; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 587 AA; 65922 MW; 06F76764B6984D52 CRC64;

Query Match 72.9%; Score 43; DB 2; Length 587;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RVYRSRDQLDL 12
 DB 267 RIRYRDLNL 278

RESULT 12
 Q52503.ORYSA PRELIMINARY; PRT; 711 AA.
 AC Q52503;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Translation initiation factor eIF-4f isoform subunit p82-
 DE like
 GN Name=OSJNB007103.22;
 OS Oryza sativa (Japanese cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

CC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RT "Oryza sativa japonica (GA3) genomic DNA, chromosome 6, BAC
 clone OSJNB007103.22,"
 RL submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005492; BAB62014.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR003890; IPR003890; IPR003890;
 DR InterPro; IPR00571; Znf_CCH.
 DR Pfam; PF02854; MIF4G; 1.
 DR Pfam; PF00642; Zf_CCH; 3.
 DR SMART; SM00543; MIF4G; 1.
 DR SMART; SM00356; Znf_CCH; 3.
 KW Initiation factor.
 SQ SEQUENCE 711 AA; 80907 MW; 2F05890B59C9D6C2 CRC64;

Query Match 72.9%; Score 43; DB 2; Length 711;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RVYRSRDQLDL 12
 DB 237 RYSYRDLNL 248

RESULT 13
 Q5A202.EMENI PRELIMINARY; PRT; 1524 AA.
 AC Q5A202;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS ORFNames=AN6228.2;
 GN Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nuebaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barua N., Bastien V., Bloom T., Boguslavsky L.,
 RA Bouhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeRellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Eriksson J., Fero S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karates A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meidert J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Notbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamaa J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wymann D., Young G., Zainoun J., Zembeck L., Zimmer A., Zody M.,
 RA Zander E.,
 RT "Genome Sequence of *Aspergillus nidulans*,"
 RL submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

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DR EMBL; AACD01000106; EAA57642.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR003169; GFF.
DR Pfam; PF02213; GFF; 1.
DR SMART; SM00444; GFF; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50829; GFF; 1.
DR Hypothetical protein; Nuclear protein.
SQ SEQUENCE 1524 AA; 161671 MW; 8BF805D0D266D4 CRC64;

Query Match 72.9%; Score 43; DB 2; Length 1524;
Best Local Similarity 80.0%; Pred. No. 93;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RYRSRDQLDL 12
Db 89 RYRSRDQLDL 98

RESULT 14
Q4VMT9_9UROC PRELIMINARY; PRT; 60 AA.
ID Q4VMT9_9UROC PRELIMINARY; PRT; 60 AA.
AC Q4VMT9;
DT 13-SEP-2005 (TRENBLREL. 31, Created)
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE Hox9 (Fragment).
GN Name:Hox9;
OS Oikopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Oikopleuridae; Oikopleura.
OX NCBI_TaxID=34765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA See H.C., Maeland A.D., Edvardsen R.B., Chourrout D.;
RT "Hypervariable and Highly Divergent Intron/Exon Organizations in The
RT Chordate Oikopleura dioica."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY294053; AA063435.1; -; Genomic_DNA.
DR InterPro; IPR01356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR000447; HTH_lambdarepressor.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 60 AA; 7739 MW; 6E183E697E15D66 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 60;
Best Local Similarity 75.0%; Pred. No. 6.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RYRSRDQLDL 12
Db 5 RYRSRDQLDL 16

RESULT 15
Q8Y1Y7_RALSO PRELIMINARY; PRT; 232 AA.
ID Q8Y1Y7_RALSO PRELIMINARY; PRT; 232 AA.
AC Q8Y1Y7;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE PROBABLE RESPONSE REGULATOR TRANSCRIPTION REGULATOR PROTEIN.

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GN OrderedLocustNames=RS050; ORFNames=RS04916;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Gentin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Broctier P., Camus J.C., Catolico L.,
RA Chandler M., Cholme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Molan A., Robert C., Saurin W., Schlex T.,
RA Siguler P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AL646059; CAD14078.1; -; Genomic_DNA.
DR HSSP; Q9WYN0; 1KGS.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:000156; F:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0000160; P:two-component signal transduction system {p. . .}; IEA.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00072; Response_reg; 1.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Complete proteome; DNA-binding; Sensory transduction; Transcription;
KW Transcription regulation; Two-component regulatory system.
SQ SEQUENCE 232 AA; 25020 MW; FB102E1671C0AA71 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 232;
Best Local Similarity 58.3%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RYRSRDQLDL 12
Db 142 RYRSRDQLDL 153

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Job time : 118.091 secs

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OM protein - protein search, using SW model

Run on: November 29, 2005, 22:45:04 ; Search time 28.6364 Seconds
(without alignments)
34.645 Million cell updates/sec

Title: US-10-019-198A-2
Perfect score: 59
Sequence: 1 RVRYSRDQLDL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
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3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	117	2	US-09-621-976-7566
2	39	66.1	60	2	US-08-751-344B-5
3	37	62.7	159	2	US-08-481-435-13
4	37	62.7	532	2	US-08-481-435-12
5	37	62.7	553	2	US-08-481-435-11
6	37	62.7	621	2	US-09-518-092-183
7	37	62.7	823	2	US-08-481-435-4
8	37	62.7	836	2	US-08-481-435-9
9	37	62.7	844	2	US-08-481-435-7
10	37	62.7	855	2	US-08-481-435-8
11	37	62.7	855	2	US-09-489-039A-12429
12	36	61.0	259	2	US-09-452-239-42
13	36	61.0	419	2	US-09-252-991A-30457
14	36	61.0	919	2	US-09-252-991A-28689
15	36	61.0	935	2	US-09-252-991A-19888
16	35	59.3	205	2	US-09-248-796A-19844
17	35	59.3	214	2	US-09-949-016-9034
18	35	59.3	214	2	US-09-949-016-9035
19	35	59.3	314	2	US-09-080-044-3
20	35	59.3	314	2	US-09-531-857A-3
21	35	59.3	509	2	US-08-688-988-40
22	35	59.3	603	2	US-09-973-457-2
23	35	59.3	2206	1	US-07-852-260-2
24	35	59.3	2206	1	US-08-461-503-2
25	35	59.3	2206	2	US-08-465-250-2
26	34	57.6	53	1	US-08-549-004A-11
27	34	57.6	53	2	US-09-051-982A-11

ALIGNMENTS

28	34	57.6	61	1	US-08-757-116C-30	Sequence 30, Appl
29	34	57.6	105	2	US-09-583-110-3678	Sequence 3678, Ap
30	34	57.6	106	2	US-09-621-976-6228	Sequence 6229, Ap
31	34	57.6	106	2	US-09-513-999C-8160	Sequence 8160, Ap
32	34	57.6	109	2	US-09-107-433-3306	Sequence 3306, Ap
33	34	57.6	113	2	US-09-640-211A-631	Sequence 631, Appl
34	34	57.6	157	2	US-09-583-110-3614	Sequence 3614, Ap
35	34	57.6	129	2	US-08-981-527A-11	Sequence 11, Appl
36	34	57.6	129	2	US-10-147-936B-11	Sequence 11, Appl
37	34	57.6	272	2	US-09-328-352-7112	Sequence 7112, Ap
38	34	57.6	283	1	US-08-583-672-2	Sequence 2, Appl1
39	34	57.6	283	1	US-08-202-044-2	Sequence 2, Appl1
40	34	57.6	283	2	US-08-751-344B-2	Sequence 2, Appl1
41	34	57.6	284	2	US-08-589-028-6	Sequence 6, Appl1
42	34	57.6	284	2	US-08-784-582-6	Sequence 6, Appl1
43	34	57.6	284	2	US-08-785-271-6	Sequence 6, Appl1
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45	34	57.6	290	2	US-09-270-767-50463	Sequence 50463, A

RESULT 1
US-09-621-976-7566
Sequence 7566, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT FILING DATE: US/09/621, 976
NUMBER OF SEQ ID NOS: 2000-07-21
SOFTWARE: Patent.pm
SEQ ID NO 7566
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-7566

Query Match 67.8%, Score 40; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
DB 76 RIKYSRDLKL 87

RESULT 2
US-08-751-344B-5
Sequence 5, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751.344B
; FILING DATE: 19-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,044
; FILING DATE: 23-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9110
; TELEFAX: (617) 345-9100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-751-344B-5

Query Match      66.1%; Score 39; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches      8; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

Qy      1 RVRYSRDQLDL 12
Db      5 RTAYRSQDLLEL 16

RESULT 3
US-08-481-435-13
; Sequence 13, Application US/08481435
; Patent No. 6027906
; GENERAL INFORMATION:
; APPLICANT: Balgansh, Tanjore S
; TITLE OF INVENTION: Town, Christine
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.435
; FILING DATE: 10-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IN 580/MAS/94
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9404072-2
; FILING DATE: 24-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
```

```

; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; IMMEDIATE SOURCE:
; CLONE: PARC 0392
; US-08-481-435-13

Query Match      62.7%; Score 37; DB 2; Length 159;
Best Local Similarity 60.0%; Pred. No. 20;
Matches      6; Conservative      4; Mismatches      0; Indels      0; Gaps      0;

Qy      3 RYSRDQLDL 12
Db      91 RYSKDRILEL 100

RESULT 4
US-08-481-435-12
; Sequence 12, Application US/08481435
; Patent No. 6027906
; GENERAL INFORMATION:
; APPLICANT: Balgansh, Tanjore S
; TITLE OF INVENTION: Town, Christine
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.435
; FILING DATE: 10-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IN 580/MAS/94
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9404072-2
; FILING DATE: 24-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; IMMEDIATE SOURCE:
; CLONE: PARC 0593 truncated soluble PBP 1B
; US-08-481-435-12
```


Query Match 62.7%; Score 37; DB 2; Length 532;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSRDQLDL 12
|||:|:|:|:
DB 279 RYSKDRILEL 288

RESULT 5

US-08-481-435-11
Sequence 11, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesch, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
CLONE: PARC 0592 truncated PBP 1B
US-08-481-435-11

Query Match 62.7%; Score 37; DB 2; Length 553;
Best Local Similarity 60.0%; Pred. No. 79;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSRDQLDL 12
|||:|:|:|:
DB 300 RYSKDRILEL 309

RESULT 6

US-09-538-092-183
Sequence 183, Application US/09538092
Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Gioc, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurataseqFormatter Version 0.9
SEQ ID NO 183

LENGTH: 621
TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

FEATURE:
NAME/KEY: misc_feature

LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number YDR292C
US-09-538-092-183

Query Match 62.7%; Score 37; DB 2; Length 621;
Best Local Similarity 54.5%; Pred. No. 90;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VRYSRDQLDL 12
|||:|:|:|:
DB 496 IYSRDQNPDI 506

RESULT 7

US-08-481-435-4
Sequence 4, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesch, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-481-435-4

Query Match 62.7%; Score 37; DB 2; Length 833;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYSDQLDL 12
|||:::|
Db 279 RYSDRLTEL 288

RESULT 8
US-08-481-435-9
Sequence 9, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganes, Tanjore S
TITLE OF INVENTION: No. 6027906e1 Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
CLONE: PARC0469 PBP 1B del 8
US-08-481-435-9

Query Match 62.7%; Score 37; DB 2; Length 836;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 RYSDQLDL 12
|||:::|
Db 292 RYSDRLTEL 301

RESULT 9
US-08-481-435-7
Sequence 7, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganes, Tanjore S
TITLE OF INVENTION: No. 6027906e1 Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 844 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
CLONE: PARC0438 PBP 1B QQA
US-08-481-435-7

Query Match 62.7%; Score 37; DB 2; Length 844;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 RYSDQLDL 12
|||:::|
Db 300 RYSDRLTEL 309

RESULT 10
US-08-481-435-8
Sequence 8, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganes, Tanjore S
TITLE OF INVENTION: No. 6027906e1 Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 844 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
CLONE: PARC0468 PBP 1B QOUL
US-08-481-435-8

Query Match 62.7%; Score 37; DB 2; Length 844;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 RYSRDQLDL 12
DB 300 RYSKRILEL 309
RESULT 11
US-09-489-039A-12429
Sequence 12429, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12429
LENGTH: 855
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12429

Query Match 62.7%; Score 37; DB 2; Length 855;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 RYSRDQLDL 12

DB 306 RYSKRILEL 315
RESULT 12
US-09-452-239-42
Sequence 42, Application US/09452239
Patent No. 6465229
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni J.
APPLICANT: Fader, Gary M.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: B81284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 42
LENGTH: 259
TYPE: PRT
ORGANISM: Triticum aestivum
US-09-452-239-42
Query Match 61.0%; Score 36; DB 2; Length 259;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 RYSRDQLDL 12
DB 221 RYRDFVLDL 231

RESULT 13
US-09-252-991A-30457
Sequence 30457, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30457
LENGTH: 419
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30457

Query Match 61.0%; Score 36; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RYSRDQL 9
DB 394 RYSRDQL 400

RESULT 14
US-09-252-991A-28689
Sequence 28689, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28689
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28689

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Query Match          61.0%; Score 36; DB 2; Length 891;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY      4 YSRDQLDL 12
        |||||
Db      562 YSRDQLFL 570

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RESULT 15
US-09-252-991A-19888
; Sequence 19888, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19888
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19888

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```

Query Match          61.0%; Score 36; DB 2; Length 935;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      1 RVRYSRDQLLD 11
        |||||
Db      88 RIRQRTQLLD 98

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Search completed: November 29, 2005, 23:04:21
 Job time : 28.6364 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: November 29, 2005, 22:52:34 (Search time 93.5455 Seconds
(without alignments)
53.599 Million cell updates/sec

Title: US-10-019-198a-2
Perfect score: 59
Sequence: 1 RVRYSRDQLDL 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	16	3	US-09-973-473-13
2	59	100.0	784	5	US-10-739-930-10656
3	53	89.8	775	4	US-10-424-599-23945
4	52	88.1	148	4	US-10-767-701-38015
5	52	88.1	234	4	US-10-425-115-223562
6	52	88.1	752	4	US-10-437-963-148037
7	52	88.1	785	4	US-10-425-115-229192
8	50	84.7	775	4	US-10-424-599-23946
9	46	78.0	789	4	US-10-424-599-231391
10	45	76.3	16	3	US-09-973-473-14
11	44	74.6	566	4	US-10-437-963-172637
12	43	72.9	719	4	US-10-437-963-199348
13	42	71.2	177	4	US-10-424-599-269495
14	42	71.2	397	4	US-10-425-114-37174
15	42	71.2	576	4	US-10-424-599-156877
16	41	69.5	717	4	US-10-320-797-3285
17	39	66.1	109	4	US-10-424-599-285588
18	39	66.1	500	6	US-11-097-143-3675
19	38	64.4	234	6	US-11-097-143-18729
20	38	64.4	240	4	US-10-424-599-156642
21	38	64.4	665	3	US-09-906-419-15
22	38	64.4	665	4	US-10-119-136-15
23	38	64.4	665	4	US-10-410-031-15
24	38	64.4	666	5	US-10-739-930-6852
25	38	64.4	852	5	US-10-732-923-23135
26	38	64.4	1516	4	US-10-437-963-187843
27	37	62.7	192	4	US-10-425-115-257529

ALIGNMENTS

28	37	62.7	245	4	US-10-369-493-11354	Sequence 11354, A
29	37	62.7	513	5	US-10-282-122A-55450	Sequence 55450, A
30	37	62.7	799	5	US-10-489-034-2	Sequence 1, Appli
31	37	62.7	822	5	US-10-489-034-1	Sequence 2, Appli
32	37	62.7	824	4	US-10-282-122A-77741	Sequence 77741, A
33	37	62.7	840	4	US-10-282-122A-75215	Sequence 75215, A
34	37	62.7	840	4	US-10-282-122A-76075	Sequence 76075, A
35	37	62.7	844	3	US-09-815-242-10039	Sequence 10039, A
36	37	62.7	844	3	US-10-282-122A-56420	Sequence 56420, A
37	37	62.7	846	3	US-09-815-242-13904	Sequence 13904, A
38	37	62.7	852	4	US-10-282-122A-60016	Sequence 60016, A
39	37	62.7	1222	5	US-10-012-697-1568	Sequence 1568, Ap
40	37	62.7	1222	5	US-10-779-543-23568	Sequence 23568, A
41	37	62.7	1502	4	US-10-369-493-13947	Sequence 13947, Ap
42	37	62.7	1812	6	US-11-097-143-858	Sequence 858, App
43	36	61.0	143	4	US-10-437-963-131881	Sequence 131881, A
44	36	61.0	143	4	US-10-335-977-8590	Sequence 8590, Ap
45	36	61.0	160	4	US-10-335-977-8591	Sequence 8591, Ap

RESULT 1
US-09-973-473-13
Sequence 13, Application US/09973473
Publication No. US20030041341A1
GENERAL INFORMATION:
APPLICANT: TREMBLAY, Nahum
APPLICANT: TSUKIYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973, 473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: wheat germ
US-09-973-473-13
Query Match 100.0%; Score 59; DB 3; Length 16;
Best Local Similarity: 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVRYSRDQLDL 12
DB 1 RVRYSRDQLDL 12
RESULT 2
US-10-739-930-10656
Sequence 10656, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 10656

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; LENGTH: 784
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(784)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CS64_1.p
US-10-739-930-10656

Query Match      100.0%; Score 59; DB 5; Length 784;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVRYSRDQLDL 12
Db      63 RVRYSRDQLDL 74

RESULT 3
US-10-424-599-239945
; Sequence 239945; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 239945
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(775)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_58696C.1.pep
US-10-424-599-239945

Query Match      89.8%; Score 53; DB 4; Length 775;
Best Local Similarity 91.7%; Pred. No. 0.88;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RVRYSRDQLDL 12
Db      58 RVRYSRDQLDL 69

RESULT 4
US-10-767-701-38015
; Sequence 38015; Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38015
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Oryza sativa
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; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C43260_1.pep
US-10-767-701-38015

Query Match      88.1%; Score 52; DB 4; Length 148;
Best Local Similarity 83.3%; Pred. No. 0.23;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVRYSRDQLDL 12
Db      61 RVRYSRDQLDL 72

RESULT 5
US-10-425-115-223562
; Sequence 223562; Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 223562
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(234)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135478C.1.pep
US-10-425-115-223562

Query Match      88.1%; Score 52; DB 4; Length 234;
Best Local Similarity 83.3%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVRYSRDQLDL 12
Db      60 RVRYSRDQLDL 71

RESULT 6
US-10-437-963-148037
; Sequence 148037; Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148037
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Oryza sativa
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FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_48508C.1.pep
US-10-437-963-148037

Query Match 88.1%; Score 52; DB 4; Length 752;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
|||:|||||
DB 61 RVRYTRDQLDL 72

RESULT 7
US-10-425-115-294192
Sequence 294192, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 294192
LENGTH: 785
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(785)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_31387C.1.pep
US-10-425-115-294192

Query Match 88.1%; Score 52; DB 4; Length 785;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
|||:|||||
DB 60 RVRYTRDQLDL 71

RESULT 8
US-10-424-599-239946
Sequence 239946, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239946
LENGTH: 775
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_58697C.1.pep
US-10-424-599-239946

Query Match 84.7%; Score 50; DB 4; Length 775;

Best Local Similarity 83.3%; Pred. No. 3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
|||:|||||
DB 60 RVRYTRDQLDL 71

RESULT 9
US-10-424-599-231391
Sequence 231391, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231391
LENGTH: 789
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_50969C.1.pep
US-10-424-599-231391

Query Match 78.0%; Score 46; DB 4; Length 789;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12
|||:|||||
DB 72 RVRYTRDQLDL 83

RESULT 10
US-09-973-473-14
Sequence 14, Application US/09973473
Publication No. US2003004131A1
GENERAL INFORMATION:
APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, Michel
APPLICANT: TSUKIYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 16
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-973-473-14

Query Match 76.3%; Score 45; DB 3; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRYSRDQLDL 12

Db 1 RVKXTRDQLL 12

RESULT 11
US-10-437-963-172637
; Sequence 172637, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172637
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70754C.1.pep
US-10-437-963-172637

Query Match 74.6%; Score 44; DB 4; Length 566;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKXTRDQLL 12
Db 140 QIRYTRDQLL 151

RESULT 12
US-10-437-963-199348
; Sequence 199348, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 199348
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94921C.1.pep
US-10-437-963-199348

Query Match 72.9%; Score 43; DB 4; Length 719;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 237 R1SYTRDQLL 248

RESULT 13
US-10-424-599-269495
; Sequence 269495, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 269495
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85374C.1.pep
US-10-424-599-269495

Query Match 71.2%; Score 42; DB 4; Length 177;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKXTRDQLL 10
Db 71 RVKXTRDQLL 80

RESULT 14
US-10-425-114-37174
; Sequence 37174, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37174
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 70086653_FLI.pep
US-10-425-114-37174

Query Match 71.2%; Score 42; DB 4; Length 397;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKXTRDQLL 12
Db 363 RLKXSRDELAL 374

RESULT 15
US-10-424-599-156877
; Sequence 156877, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156877
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(576)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112682C.1.pdp
US-10-424-599-156877

Query Match 71.2%; Score 42; DB 4; Length 576;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYRYGRDQLDL 12
DB 542 RLKYSRDELAL 553

Search completed: November 29, 2005, 23:10:27
Job time : 94.5455 secs

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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:45:19 ; Search time 3 Seconds
(without alignments)
12.124 Million cell updates/sec

Title: US-10-019-198a-2
Perfect score: 59
Sequence: 1 RYRYSRDQLDL 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	59.3	495	1 US-10-467-962B-93	Sequence 93, Appl
2	35	55.9	1263	1 US-10-485-517-127	Sequence 127, Appl
3	32	54.2	396	7 US-11-061-869-17	Sequence 17, Appl
4	31	52.5	18	7 US-11-054-515-3040	Sequence 3040, Ap
5	31	52.5	253	7 US-11-054-515-1636	Sequence 1636, Ap
6	31	52.5	415	1 US-10-793-626-1406	Sequence 1406, Ap
7	31	52.5	495	1 US-10-821-234-1154	Sequence 1154, Ap
8	31	52.5	537	1 US-10-793-626-1712	Sequence 1712, Ap
9	31	52.5	775	1 US-10-131-826A-120	Sequence 120, App
10	31	52.5	834	1 US-10-131-826A-148	Sequence 148, App
11	31	52.5	867	1 US-10-131-826A-20	Sequence 20, Appl
12	30	50.8	138	1 US-10-793-626-1540	Sequence 1540, Ap
13	30	50.8	176	1 US-10-793-626-2328	Sequence 2328, Ap
14	30	50.8	176	1 US-10-793-626-612	Sequence 612, App
15	30	50.8	286	1 US-10-793-626-2192	Sequence 2192, App
16	30	50.8	312	1 US-10-858-730-117	Sequence 117, App
17	30	50.8	323	1 US-10-821-234-981	Sequence 981, App
18	29.5	50.0	512	7 US-11-012-762-64	Sequence 64, Appl
19	29	49.2	129	1 US-10-821-234-1195	Sequence 1195, Ap
20	29	49.2	238	7 US-11-074-176-148	Sequence 148, Appl
21	29	49.2	284	1 US-10-510-386-72	Sequence 72, Appl
22	29	49.2	366	7 US-11-061-869-11	Sequence 11, Appl
23	29	49.2	406	1 US-10-821-234-1026	Sequence 1026, Ap
24	29	49.2	502	1 US-10-793-626-3136	Sequence 3136, Ap
25	29	49.2	552	7 US-11-074-176-204	Sequence 204, App

26	29	49.2	1067	7 US-11/062	Sequence 3, Appl
27	29	49.2	1092	7 US-11/062	Sequence 6, Appl
28	29	49.2	1227	7 US-10-793-626-96	Sequence 96, Appl
29	29	49.2	1400	1 US-10-821-234-1045	Sequence 1045, Ap
30	28.5	48.3	1158	1 US-10-858-730-70	Sequence 70, Appl
31	28.5	48.3	1170	1 US-10-858-730-71	Sequence 71, Appl
32	28	47.5	93	1 US-10-667-295-52	Sequence 52, Appl
33	28	47.5	96	7 US-11-053-076-80	Sequence 80, Appl
34	28	47.5	250	7 US-11-054-515-1022	Sequence 1022, Ap
35	28	47.5	305	1 US-10-793-626-436	Sequence 436, App
36	28	47.5	306	7 US-11-039-722-4	Sequence 4, App
37	28	47.5	308	1 US-10-821-234-1001	Sequence 1001, Ap
38	28	47.5	371	1 US-10-467-962B-41	Sequence 41, Ap
39	28	47.5	420	1 US-10-793-626-2296	Sequence 2296, Ap
40	28	47.5	424	1 US-10-793-626-2896	Sequence 2896, Ap
41	28	47.5	496	1 US-10-486-968-52	Sequence 52, Appl
42	28	47.5	555	1 US-10-131-826A-72	Sequence 72, Appl
43	28	47.5	626	7 US-11-082-389-392	Sequence 392, Appl
44	28	47.5	634	7 US-11-082-389-390	Sequence 390, App
45	28	47.5	634	7 US-11-082-389-390	Sequence 390, App

ALIGNMENTS

```
RESULT 1
US-10-467-962B-93
; Sequence 93, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467, 962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 93
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-93

Query Match      59.3%; Score 35; DB 1; Length 495;
Best Local Similarity 58.3%; Pred. No. 7.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RYRYSRDQLDL 12
Db      422 RKVYRDVQL 433

RESULT 2
US-10-485-517-127
; Sequence 127, Application US/10485517
; Publication No. US20050256289A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485, 517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
```

;; PRIOR FILING DATE: 2002-01-09
;; NUMBER OF SEQ ID NOS: 424
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 127
;; LENGTH: 1263
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-10-485-517-127

Query Match 55.9%; Score 33; DB 1; Length 1263;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 YSRDQLDL 12
Db 401 YSRDQLDL 409

RESULT 3
US-11-061-869-17
; Sequence 17, Application US/11061869
; Publication No. US20050256074A1
; GENERAL INFORMATION:
; APPLICANT: Crumpton, T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING LYMPHOCYTE ACTIVITY
; FILE REFERENCE: CIBT-P01-080
; CURRENT APPLICATION NUMBER: US/11/061,869
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US/09/724,964
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,112
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-869-17

OY 1 RRYARKQVPL 12
Db 32 RRYARKQVPL 43

Query Match 54.2%; Score 32; DB 7; Length 396;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 4
US-11-054-515-3040
; Sequence 3040, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 3040
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-3040

Query Match 52.5%; Score 31; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 1,1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSRDQLDL 11
Db 10 YMRDELDD 17

RESULT 5
US-11-054-515-1636
; Sequence 1636, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1636
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1636

Query Match 52.5%; Score 31; DB 7; Length 253;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSRDQLDL 11
Db 108 YMRDELDD 115

RESULT 6
US-10-793-626-1406
; Sequence 1406, Application US/10793626

```
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P0348005
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1406
LENGTH: 415
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
FEATURE:
OTHER INFORMATION: amino acid sequence
NAME/KEY: MOD RES
LOCATION: (415)
OTHER INFORMATION: variable amino acid
US-10-793-626-1406

Query Match      52.5%; Score 31; DB 1; Length 415;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RYSRDQL 9
        |||::|||:
Db      21 RYSRDEM 27

RESULT 7
US-10-821-234-1154
Sequence 1154, Application US/10821234
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC SEQ_Genes Version 1.0
SEQ ID NO 1154
LENGTH: 495
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1154

Query Match      52.5%; Score 31; DB 1; Length 495;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 RYRYSRDQLD 11
        |||::|||:
Db      200 RYDVERNDL 210

RESULT 8
US-10-793-626-1712
Sequence 1712, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P0348005
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1712
LENGTH: 537
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-1712

Query Match      52.5%; Score 31; DB 1; Length 537;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 RYSRDQLD 12
        |||::|||:
Db      309 RYTKQNLDI 318

RESULT 9
US-10-131-826A-120
Sequence 120, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C126
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remainig Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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SEQ ID NO 120
LENGTH: 775
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-120

Query Match 52.5%; Score 31; DB 1; Length 775;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VRYSRDQL 9
Db 702 RLKXTHDQL 710

RESULT 10
US-10-131-826A-148
Sequence 148, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 148
LENGTH: 834
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-148

Query Match 52.5%; Score 31; DB 1; Length 834;
Best Local Similarity 54.5%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 VRYSRDQLDL 12
Db 287 IREHRRLLEL 297

RESULT 11
US-10-131-826A-20
Sequence 20, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059164
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 20
LENGTH: 867
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-20

Query Match 52.5%; Score 31; DB 1; Length 867;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 YSRDQLDL 12
Db 187 YSKDYLTDL 195

RESULT 12
US-10-793-626-1540
Sequence 1540, Application US/10793626

```
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 1540
/ LENGTH: 138
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-1540
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```
Query Match          50.8%; Score 30; DB 1; Length 138;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      4 YSRDQLDL 12
      |||:|:|
DB      116 YSDDELADL 124
```

```
RESULT 13
US-10-793-626-2328
/ Sequence 2328, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 2328
/ LENGTH: 145
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-2328
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```
Query Match          50.8%; Score 30; DB 1; Length 145;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 YSRDQLDL 12
      |||:|:|
DB      85 YSDDELADL 93
```

```
RESULT 14
US-10-793-626-612
/ Sequence 612, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
```

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/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 612
/ LENGTH: 176
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-612
```

```
Query Match          50.8%; Score 30; DB 1; Length 176;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      4 YSRDQLDL 12
      |||:|:|
DB      116 YSDDELADL 124
```

```
RESULT 15
US-10-793-626-2192
/ Sequence 2192, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 2192
/ LENGTH: 286
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-2192
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```
Query Match          50.8%; Score 30; DB 1; Length 286;
Best Local Similarity 41.7%; Pred. No. 34;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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QY      1 RVRYSRDQLDL 12
      |::|:|:|
DB      267 RIQYVNDLQDI 278
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Job time : 4.25 secs
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GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: November 29, 2005, 21:58:13 ; Search time 95.4546 Seconds
(without alignments)
46.030 Million cell updates/sec

Title: US-10-019-198A-3
Perfect score: 47
Sequence: 1 RIIDYRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003s:*
- 7: geneseqp2003b:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	97.9	9	5	ABB96919
2	46	97.9	9	5	ABB97044
3	46	97.9	9	6	ABR84356
4	46	97.9	10	4	ABR31440
5	46	97.9	12	4	ABR31448
6	46	97.9	12	4	ABR31449
7	46	97.9	16	3	ABR11093
8	46	97.9	16	3	ABR11094
9	46	97.9	16	3	ABR11095
10	46	97.9	16	3	ABR11099
11	46	97.9	16	3	ABR11085
12	46	97.9	16	3	ABR11088
13	46	97.9	16	3	ABR11086
14	46	97.9	16	3	ABR11087
15	46	97.9	16	4	ABR84404
16	46	97.9	16	4	ABR84393
17	46	97.9	16	4	ABR84395
18	46	97.9	16	4	ABR84396
19	46	97.9	16	4	ABR84394
20	46	97.9	100	2	AAW98920
21	46	97.9	100	2	AAW94466
22	46	97.9	100	7	ABR57347
23	46	97.9	117	5	ABR57347
24	46	97.9	117	7	ABR57347

25	46	97.9	117	7	ADG62056
26	46	97.9	117	8	ADJ76365
27	46	97.9	117	9	ABR95265
28	46	97.9	117	9	ABR95264
29	46	97.9	117	9	ABR95266
30	46	97.9	118	2	AAW94274
31	46	97.9	118	5	AAW96147
32	46	97.9	118	5	ABG31601
33	46	97.9	118	5	ABR97146
34	46	97.9	118	7	ADD18622
35	46	97.9	118	7	ADG62054
36	46	97.9	118	7	ADG62058
37	46	97.9	118	8	ADJ75665
38	46	97.9	118	8	ADP25252
39	46	97.9	118	9	ADX05722
40	46	97.9	118	9	ADY17812
41	46	97.9	118	9	ABR95263
42	46	97.9	119	3	ABR56689
43	46	97.9	120	2	AAW94275
44	46	97.9	120	3	AAW96148
45	46	97.9	120	5	ABG31602

ALIGNMENTS

RESULT 1
ABB96919 standard; peptide; 9 AA.

ABB96919;

21-JUN-2002 (first entry)

Human tumour antigen related peptide SEQ ID NO 14.

Human; tumour; antigen; HLA-A2; cytotoxic T cell; cytostatic; cancer;

vaccine.

Homo sapiens.

MO200210369-A1.

07-FEB-2002.

30-JUL-2001; 2001WO-JP006526.

31-JUL-2000; 2000JP-00231814.

(ITOH/) ITOH K.

Itoh K;

WPI; 2002-291857/33.

Tumour antigens inducing and/or activating HLA-A2-restricted tumor-specific cytotoxic T cells, useful in diagnosis of and screening drugs e.g. cancer vaccines for specific treatment of pancreatic cancer.

Claim 1; Page 21; 127pp; Japanese.

The invention relates to a peptide comprising an amino acid sequence selected from 44 fully defined amino acid sequences (ABB96906-ABB96549) and a polypeptide comprising an amino acid sequence selected from the 9 fully defined amino acid sequences (ABB97143-ABB97151). The above comprise a tumour antigen inducing or activating HLA-A2-restricted tumour-specific cytotoxic T cells, which recognise HLA-A2 and a tumour antigen peptide and is thus activated. The peptides and polypeptides have cytostatic activity. The tumour antigen is useful in diagnosis of and screening drugs for specific treatment of pancreatic cancer, colon cancer and stomach cancer including in the form of vaccines. The present sequence is that of a tumour antigen peptide, useful to the invention

SQ Sequence 9 AA;

Query Match 97.9%; Score 46; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
 |||||
 Db 1 RIYDRKFL 9

RESULT 2
 ABB97044
 ID ABB97044 standard; peptide; 9 AA.
 XX
 AC ABB97044;
 XX
 DT 21-JUN-2002 (first entry)
 XX
 DE Human tumour antigen related peptide 95.
 XX
 KM Human; tumour; antigen; HLA-A2; cytotoxic T cell; cytostatic; cancer;
 KM vaccine.
 KM
 KW Homo sapiens.
 XX
 OS
 PN WO200210369-A1.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-JP006526.
 XX
 PR 31-JUL-2000; 2000JP-00231814.
 XX
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K;
 XX
 DR WPI; 2002-291857/33.
 XX
 PT Tumor antigens inducing and/or activating HLA-A2-restricted tumor-
 specific cytotoxic T cells, useful in diagnosis of and screening drugs
 e.g. cancer vaccines for specific treatment of pancreatic cancer.
 XX
 PS Example 4; Fig 8; 127pp; Japanese.
 XX
 CC The invention relates to a peptide comprising an amino acid sequence
 CC selected from 44 fully defined amino acid sequences (ABB96906-ABB969549)
 CC and a polypeptide comprising an amino acid sequence selected from the 9
 CC fully defined amino acid sequences (ABB97143-ABB97151). The above
 CC comprise a tumour antigen inducing or activating HLA-A2-restricted tumour
 CC -specific cytotoxic T cells, which recognise HLA-A2 and a tumour antigen
 CC peptide and is thus activated. The peptides and polypeptides have
 CC cytostatic activity. The tumour antigen is useful in diagnosis of and
 CC screening drugs for specific treatment of pancreatic cancer, colon cancer
 CC and stomach cancer including in the form of vaccines. The present
 CC sequence is that of a tumour antigen peptide, useful to the invention
 XX
 SQ Sequence 9 AA;

Query Match 97.9%; Score 46; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
 |||||
 Db 1 RIYDRKFL 9

RESULT 3
 ABR84356
 ID ABR84356 standard; peptide; 9 AA.

AC ABR84356;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human EIF4E-BP HLA-A2 epitope, SEQ ID NO:7.
 XX
 KM Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 KM cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 KM immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 KM human; human leukocyte antigen; HLA-A2 epitope.
 XX
 OS
 PN JP2002365286-A.
 XX
 PD 18-DEC-2002.
 XX
 PF 18-SEP-2001; 2001JP-00283413.
 XX
 PR 13-NOV-2000; 2000JP-00345094.
 XX
 PA (ITOY/) ITO Y.
 XX
 DR WPI; 2003-508315/48.
 XX
 PT A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX
 PS Example 7; Page 8; 18pp; Japanese.
 XX
 CC The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention
 XX
 SQ Sequence 9 AA;

Query Match 97.9%; Score 46; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
 |||||
 Db 1 RIYDRKFL 9

RESULT 4
 AAB31440
 ID AAB31440 standard; peptide; 10 AA.
 XX
 AC AAB31440;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE A human eukaryotic Initiation Factor 4E (eIF4E) binding peptide.
 XX
 KM Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
 KM cell death; cell apoptosis; anticancer; antitumor.
 XX
 OS
 PN Homo sapiens.
 XX
 FH Key Location/Qualifiers

```

FT  Misc-difference 10
XX  /label= Lys, Met
XX  WO200078803-A2.
XX  28-DEC-2000.
XX  21-JUN-2000; 2000WO-GB002414.
XX  21-JUN-1999; 99GB-00014480.
XX  (UYDU-) UNIV DUNDEE.
XX  Proud CG, Herbert TP, Lane DP, Fahraeus R;
XX  WPI; 2001-071386/08.
XX  Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
XX  binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
XX  for inducing apoptosis in e.g. mammalian tumor cells.
XX  Claim 6; Page 31; 46pp; English.
XX  The present sequence represents a binding peptide for an eukaryotic
XX  Initiation Factor 4E (eIF4E) protein. The specification describes eIF4G
XX  and eIF4E binding agents, such as peptides or peptidomimetics. These
XX  binding agents are used for the induction of cell death. The binding
XX  peptides are used for inducing cell apoptosis. They are used in
XX  pharmaceutical compositions for anticancer or antitumor treatment of
XX  mammalian cells. Specifically, the peptides result in growth inhibition
XX  of, or increased cytotoxicity to tumour cells
XX  Sequence 10 AA;

Query Match          97.9%; Score 46; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 RIYDRKFL 9
DB  1 RIYDRKFL 9

RESULT 5
AAB31448
ID  AAB31448 standard; peptide; 12 AA.
XX  AAB31448;
XX  20-APR-2001 (first entry)
XX  A human eukaryotic Initiation Factor 4E (eIF4E) binding peptide.
XX  Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
XX  cell death; cell apoptosis; anticancer; antitumor.
XX  Homo sapiens.
XX  Key Location/Qualifiers
XX  Misc-difference 12
XX  /note= "unspecified residue given as U in the
XX  specification"
XX  WO200078803-A2.
XX  28-DEC-2000.
XX  21-JUN-2000; 2000WO-GB002414.
XX  21-JUN-1999; 99GB-00014480.
XX  (UYDU-) UNIV DUNDEE.
XX

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PI  Proud CG, Herbert TP, Lane DP, Fahraeus R;
XX  WPI; 2001-071386/08.
XX  Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
XX  binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
XX  for inducing apoptosis in e.g. mammalian tumor cells.
XX  Example; Fig 5; 46pp; English.
XX  The present sequence represents a binding peptide for an eukaryotic
XX  Initiation Factor 4E (eIF4E) protein. The specification describes eIF4G
XX  and eIF4E binding agents, such as peptides or peptidomimetics. These
XX  binding agents are used for the induction of cell death. The binding
XX  peptides are used for inducing cell apoptosis. They are used in
XX  pharmaceutical compositions for anticancer or antitumor treatment of
XX  mammalian cells. Specifically, the peptides result in growth inhibition
XX  of, or increased cytotoxicity to tumour cells
XX  Sequence 12 AA;

Query Match          97.9%; Score 46; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 RIYDRKFL 9
DB  1 RIYDRKFL 9

RESULT 6
AAB31449
ID  AAB31449 standard; peptide; 12 AA.
XX  AAB31449;
XX  20-APR-2001 (first entry)
XX  A human eukaryotic Initiation Factor 4E (eIF4E) binding peptide.
XX  Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E;
XX  cell death; cell apoptosis; anticancer; antitumor.
XX  Homo sapiens.
XX  WO200078803-A2.
XX  28-DEC-2000.
XX  21-JUN-2000; 2000WO-GB002414.
XX  21-JUN-1999; 99GB-00014480.
XX  (UYDU-) UNIV DUNDEE.
XX  Proud CG, Herbert TP, Lane DP, Fahraeus R;
XX  WPI; 2001-071386/08.
XX  Use of eukaryotic Initiation Factor 4E (eIF4E) binding agents e.g. eIF4E-
XX  binding peptide (eIF4E-BP) derivatives as anticancer or antitumor agents
XX  for inducing apoptosis in e.g. mammalian tumor cells.
XX  Example; Fig 5; 46pp; English.
XX  The present sequence represents a binding peptide for an eukaryotic
XX  Initiation Factor 4E (eIF4E) protein. The specification describes eIF4G
XX  and eIF4E binding agents, such as peptides or peptidomimetics. These
XX  binding agents are used for the induction of cell death. The binding
XX  peptides are used for inducing cell apoptosis. They are used in
XX  pharmaceutical compositions for anticancer or antitumor treatment of
XX  mammalian cells. Specifically, the peptides result in growth inhibition
XX  of, or increased cytotoxicity to tumour cells

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XX SQ Sequence 12 AA;
Query Match 97.9%; Score 46; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
    |||||
    1 RIYDRKFL 9

Db 1 RIYDRKFL 9

RESULT 7
AAB11093
ID AAB11093 standard; peptide; 16 AA.
AC AAB11093;
XX 16-FEB-2001 (first entry)
DT
XX Human eIF-4E recognition motif peptide h4E-BP1.
DE
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
KW knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
XX Homo sapiens.
XX
XX WO200060932-A1.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-CA000388.
XX
XX 09-APR-1999; 99US-0128559P.
XX 02-FEB-2000; 2000US-0179743P.
XX (UYMC-) UNIV MCGILL.
XX
XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
XX WPI; 2000-672657/65.
XX
XX Non-human transgenic animal useful as model for studying lipid and
XX glucose metabolism, has germ and somatic cells containing knockout
XX mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
XX 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (I) whose
XX germ cells and somatic cells contain a knockout mutation in DNA encoding
XX a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
XX protein 1) shows a phenotype of an altered glucose and/or fat metabolism
XX when compared to a control animal. The products of the invention have
XX antidiabetic and anorectic activity. The non-human transgenic animals are
XX useful as models for the investigation of lipid and glucose metabolism,
XX energy homeostasis and associated diseases. The transgenic animals are
XX also useful for selection and identification of modulators of the
XX expression and/or activity of 4E-BP1 and for screening drugs to isolate
XX therapeutic agents which are useful as anti-obesity, anti-fat deposition
XX disorder, anti-diabetes and anti-metabolic diseases associated with fat
XX deposition disorders. The effect of the disruption of 4E-BP1 in the
XX knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
XX tissue growth, glucose metabolism and weight gain in an animal
XX
XX Sequence 16 AA;
Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
    |||||
    1 RIYDRKFL 9

Db 1 RIYDRKFL 9

RESULT 9
AAB11095
ID AAB11095 standard; peptide; 16 AA.
XX

```

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Db 1 RIYDRKFL 9
    |||||
    1 RIYDRKFL 9

RESULT 8
AAB11094
ID AAB11094 standard; peptide; 16 AA.
AC AAB11094;
XX 16-FEB-2001 (first entry)
DT
XX Human eIF-4E recognition motif peptide h4E-BP2.
DE
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
KW knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
XX Homo sapiens.
XX
XX WO200060932-A1.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-CA000388.
XX
XX 09-APR-1999; 99US-0128559P.
XX 02-FEB-2000; 2000US-0179743P.
XX (UYMC-) UNIV MCGILL.
XX
XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
XX WPI; 2000-672657/65.
XX
XX Non-human transgenic animal useful as model for studying lipid and
XX glucose metabolism, has germ and somatic cells containing knockout
XX mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
XX 1.
XX
XX Disclosure; Fig 7; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (I) whose
XX germ cells and somatic cells contain a knockout mutation in DNA encoding
XX a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
XX protein 1) shows a phenotype of an altered glucose and/or fat metabolism
XX when compared to a control animal. The products of the invention have
XX antidiabetic and anorectic activity. The non-human transgenic animals are
XX useful as models for the investigation of lipid and glucose metabolism,
XX energy homeostasis and associated diseases. The transgenic animals are
XX also useful for selection and identification of modulators of the
XX expression and/or activity of 4E-BP1 and for screening drugs to isolate
XX therapeutic agents which are useful as anti-obesity, anti-fat deposition
XX disorder, anti-diabetes and anti-metabolic diseases associated with fat
XX deposition disorders. The effect of the disruption of 4E-BP1 in the
XX knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
XX tissue growth, glucose metabolism and weight gain in an animal
XX
XX Sequence 16 AA;
Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
    |||||
    1 RIYDRKFL 9

Db 1 RIYDRKFL 9

RESULT 9
AAB11095
ID AAB11095 standard; peptide; 16 AA.
XX

```

AC AAB11095;
 XX 16-FEB-2001 (first entry)
 DT
 XX
 DE Human eIF-4E recognition motif peptide h4E-BP3.
 XX
 XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
 KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
 KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200060932-A1.
 XX
 XX 19-OCT-2000.
 PD
 XX 07-APR-2000; 2000WO-CA000388.
 PF
 XX 09-APR-1999; 99US-0128559P.
 PR 02-FEB-2000; 2000US-0179743P.
 XX
 XX (UWMC-) UNIV MCGILL.
 PA
 XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
 PI
 XX WPI: 2000-672657/65.
 DR
 XX Non-human transgenic animal useful as model for studying lipid and
 PT glucose metabolism, has germ and somatic cells containing knockout
 PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
 PT 1.
 XX
 PS Disclosure; Fig 7; 80pp; English.
 XX
 XX This invention describes a novel non-human transgenic animal (I) whose
 CC germ cells and somatic cells contain a knockout mutation in DNA encoding
 CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
 CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
 CC when compared to a control animal. The products of the invention have
 CC antidiabetic and anorectic activity. The non-human transgenic animals are
 CC useful as models for the investigation of lipid and glucose metabolism,
 CC energy homeostasis and associated diseases. The transgenic animals are
 CC also useful for selection and identification of modulators of the
 CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
 CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
 CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
 CC deposition disorders. The effect of the disruption of 4E-BP1 in the
 CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
 CC tissue growth, glucose metabolism and weight gain in an animal
 CC
 XX
 SO Sequence 16 AA;
 Query Match 97.9%; Score 46; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIYYDRKFL 9
 DB 1 RIYYDRKFL 9
 AC AAB11099;
 XX 16-FEB-2001 (first entry)
 DT
 XX
 DE Chicken eIF-4E recognition motif peptide 4E-BP.
 XX
 XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
 KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
 KM

KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
 XX
 XX Gallus sp.
 OS
 XX WO200060932-A1.
 XX
 XX 19-OCT-2000.
 PD
 XX 07-APR-2000; 2000WO-CA000388.
 PF
 XX 09-APR-1999; 99US-0128559P.
 PR 02-FEB-2000; 2000US-0179743P.
 XX
 XX (UWMC-) UNIV MCGILL.
 PA
 XX Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
 PI
 XX WPI: 2000-672657/65.
 DR
 XX Non-human transgenic animal useful as model for studying lipid and
 PT glucose metabolism, has germ and somatic cells containing knockout
 PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
 PT 1.
 XX
 PS Disclosure; Fig 7; 80pp; English.
 XX
 XX This invention describes a novel non-human transgenic animal (I) whose
 CC germ cells and somatic cells contain a knockout mutation in DNA encoding
 CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
 CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
 CC when compared to a control animal. The products of the invention have
 CC antidiabetic and anorectic activity. The non-human transgenic animals are
 CC useful as models for the investigation of lipid and glucose metabolism,
 CC energy homeostasis and associated diseases. The transgenic animals are
 CC also useful for selection and identification of modulators of the
 CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
 CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
 CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
 CC deposition disorders. The effect of the disruption of 4E-BP1 in the
 CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
 CC tissue growth, glucose metabolism and weight gain in an animal
 CC
 XX
 SO Sequence 16 AA;
 Query Match 97.9%; Score 46; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIYYDRKFL 9
 DB 1 RIYYDRKFL 9
 AC AAB11085;
 XX 16-FEB-2001 (first entry)
 DT
 XX
 DE eIF-4E recognition motif peptide h4E-BP1.
 XX
 XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
 KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
 KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
 XX
 OS Unidentified.
 XX
 XX WO200060932-A1.
 XX
 XX 19-OCT-2000.
 PD

PF 07-APR-2000; 2000WO-CA000388.
XX
PR 09-APR-1999; 99US-0128559P.
PR 02-FEB-2000; 2000US-0179743P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sorenberg N, Tremblay M, Tsukiyama-Kohara K;
XX WPI; 2000-672657/65.
DR
XX
XX Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
1.
XX
PS Disclosure; Fig 6; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (1) whose
CC germ cells and somatic cells contain a knockout mutation in DNA encoding
CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
CC when compared to a control animal. The products of the invention have
CC antidiabetic and anorectic activity. The non-human transgenic animals are
CC useful as models for the investigation of lipid and glucose metabolism,
CC energy homeostasis and associated diseases. The transgenic animals are
CC also useful for selection and identification of modulators of the
CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
CC deposition disorders. The effect of the disruption of 4E-BP1 in the
CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
CC tissue growth, glucose metabolism and weight gain in an animal
XX
SQ Sequence 16 AA:
Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RIYDRKFL 9
Db 1 RIYDRKFL 9
AA11088
ID AAB11088 standard; peptide; 16 AA.
XX
AC AAB11088;
XX
DT 16-FEB-2001 (first entry)
XX
DE eIF-4E recognition motif peptide g94E-BP.
XX
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
OS Unidentified.
XX
PN WO200060932-A1.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-CA000388.
XX
PR 09-APR-1999; 99US-0128559P.
PR 02-FEB-2000; 2000US-0179743P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sorenberg N, Tremblay M, Tsukiyama-Kohara K;

XX
DR WPI; 2000-672657/65.
XX
PT Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
1.
XX
PS Disclosure; Fig 6; 80pp; English.
XX
XX This invention describes a novel non-human transgenic animal (1) whose
CC germ cells and somatic cells contain a knockout mutation in DNA encoding
CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
CC when compared to a control animal. The products of the invention have
CC antidiabetic and anorectic activity. The non-human transgenic animals are
CC useful as models for the investigation of lipid and glucose metabolism,
CC energy homeostasis and associated diseases. The transgenic animals are
CC also useful for selection and identification of modulators of the
CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
CC deposition disorders. The effect of the disruption of 4E-BP1 in the
CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
CC tissue growth, glucose metabolism and weight gain in an animal
XX
SQ Sequence 16 AA:
Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RIYDRKFL 9
Db 1 RIYDRKFL 9
AA11086
ID AAB11086 standard; peptide; 16 AA.
XX
AC AAB11086;
XX
DT 16-FEB-2001 (first entry)
XX
DE eIF-4E recognition motif peptide h4E-BP2.
XX
XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
KM knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
KM drug; anti-obesity; anti-fat deposition; anti-metabolic.
XX
OS Unidentified.
XX
PN WO200060932-A1.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-CA000388.
XX
PR 09-APR-1999; 99US-0128559P.
PR 02-FEB-2000; 2000US-0179743P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sorenberg N, Tremblay M, Tsukiyama-Kohara K;
XX WPI; 2000-672657/65.
DR
XX
XX Non-human transgenic animal useful as model for studying lipid and
PT glucose metabolism, has germ and somatic cells containing knockout
PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
1.

PS Disclosure; Fig 6; 80pp; English.

CC This invention describes a novel non-human transgenic animal (1) whose
 CC germ cells and somatic cells contain a knockout mutation in DNA encoding
 CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
 CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
 CC when compared to a control animal. The products of the invention have
 CC antidiabetic and anorectic activity. The non-human transgenic animals are
 CC useful as models for the investigation of lipid and glucose metabolism,
 CC energy homeostasis and associated diseases. The transgenic animals are
 CC also useful for selection and identification of modulators of the
 CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
 CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
 CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
 CC deposition disorders. The effect of the disruption of 4E-BP1 in the
 CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
 CC tissue growth, glucose metabolism and weight gain in an animal

CC XX

SQ Sequence 16 AA;

Query Match 97.9%; Score 46; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
 |||||
 1 RIYDRKFL 9

DB 1 RIYDRKFL 9

RESULT 14
 AAB11087
 ID AAB11087 standard; peptide; 16 AA.

AC AAB11087;
 16-FEB-2001 (first entry)
 eIF-4E recognition motif peptide h4E-BP3.

XX Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic;
 XX knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
 XX drug; anti-obesity; anti-fat deposition; anti-metabolic.

OS Unidentified.
 WO200060932-A1.

XX 19-OCT-2000.
 PD 07-APR-2000; 2000WO-CA000388.

XX 09-APR-1999; 99US-0128559P.
 PR 02-FEB-2000; 2000US-0179743P.

XX (UYMC-) UNIV MCGILL.
 PA Sonenberg N, Tremblay M, Tsukiyama-Kohara K;
 PI WPI; 2000-672657/65.

XX Non-human transgenic animal useful as model for studying lipid and
 PT glucose metabolism, has germ and somatic cells containing knockout
 PT mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
 PT 1.

XX Disclosure; Fig 6; 80pp; English.

XX This invention describes a novel non-human transgenic animal (1) whose
 CC germ cells and somatic cells contain a knockout mutation in DNA encoding
 CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
 CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism
 CC when compared to a control animal. The products of the invention have
 CC antidiabetic and anorectic activity. The non-human transgenic animals are

CC useful as models for the investigation of lipid and glucose metabolism,
 CC energy homeostasis and associated diseases. The transgenic animals are
 CC also useful for selection and identification of modulators of the
 CC expression and/or activity of 4E-BP1 and for screening drugs to isolate
 CC therapeutic agents which are useful as anti-obesity, anti-fat deposition
 CC disorder, anti-diabetes and anti-metabolic diseases associated with fat
 CC deposition disorders. The effect of the disruption of 4E-BP1 in the
 CC knockout mice demonstrates that an alteration of 4E-BP1 can modulate fat
 CC tissue growth, glucose metabolism and weight gain in an animal

CC XX

SQ Sequence 16 AA;

Query Match 97.9%; Score 46; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
 |||||
 1 RIYDRKFL 9

DB 1 RIYDRKFL 9

RESULT 15
 AAB84404
 ID AAB84404 standard; peptide; 16 AA.

AC AAB84404;
 22-AUG-2001 (first entry)
 4E-binding site of a 4E-binding protein.

XX 4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance;
 XX cap-dependent translation initiation repressor; apoptosis;
 XX translation initiation factor; eIF4E; Ras; cancer.

OS Gallus sp.
 WO200140293-A2.

XX 07-JUN-2001.
 PD 01-DEC-2000; 2000WO-CA001465.

XX 02-DEC-1999; 99US-0168398P.
 PR (UYMC-) UNIV MCGILL.
 PA (MINU) UNIV MINNESOTA.

XX Sonenberg N, Gingras A, Polunavsky VA, Bitterman PB;
 PI WPI; 2001-381379/40.

XX Inducing apoptosis in a cell in which the apoptosis pathway is inhibited,
 PT useful for treating cancer or highly proliferative cells, comprises
 PT decreasing the amount of eIF4F pre-initiation complex, relieving an
 PT apoptosis block.

XX Disclosure; Fig 6; 80pp; English.

XX AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is
 CC a repressor of cap-dependent translation initiation, and selectively
 CC activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-
 CC induced chemoresistance. The effects of 4E-BP1 are strictly dependent on
 CC its ability to sequester the translation initiation factor eIF4E, thereby
 CC preventing its assembly into an active pre-initiation complex. The
 CC specification describes a method for inducing apoptosis in a cell in
 CC which the apoptosis pathway is inhibited. The method comprises decreasing
 CC the amount of eIF4F pre-initiation complex by sequestration of eIF4E,
 CC thus relieving an apoptosis block. The method is useful for modulating
 CC pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-
 CC transformed cells. Thus, the method is particularly useful for treating
 CC cancer. The eIF4E sequestering agent, 4E-BP1 or its eIF4E binding portion
 CC is useful for treating high proliferative cells

XX
SQ Sequence 16 AA;

Query Match 97.9%; Score 46; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
|||
Db 1 RIYDRKFL 9

Search completed: November 29, 2005, 22:52:18
Job time : 96.4546 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:35:24 ; Search time 15.6818 Seconds
(without alignments)
61.356 Million cell updates/sec

Title: US-10-019-198a-3
Perfect score: 47
Sequence: 1 RIYDRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	97.9	117	2 A57396	PHAS-I protein - m
2	46	97.9	117	2 A55258	insulin-stimulated
3	46	97.9	118	2 S50866	translational initia
4	46	97.9	120	2 S50867	4E-BF2 protein - h
5	37	78.7	898	1 DJBPT4	DNA-directed DNA p
6	35	74.5	1680	2 A43434	furin (EC 3.4.21.7
7	34	72.3	162	1 Z3BPL7	gene 3 protein - p
8	34	72.3	281	2 A85017	hypothetical prote
9	34	72.3	531	2 B96966	beta-mannanase Man
10	34	72.3	1028	2 T01714	hypothetical prote
11	34	72.3	1251	2 B86194	hypothetical prote
12	33	70.2	107	2 D90955	hypothetical prote
13	33	70.2	107	2 A85804	hypothetical prote
14	33	70.2	107	2 H64853	hypothetical prote
15	33	70.2	120	2 F69673	hypothetical prote
16	33	70.2	162	2 Z3BPT2	gene 3 protein - p
17	33	70.2	344	2 E83383	probable transcrip
18	33	70.2	362	2 F90441	ABC transporter, A
19	33	70.2	382	2 B71303	conserved hypochet
20	33	70.2	478	2 T35402	probable phytoene
21	33	70.2	612	2 T39666	MD-repeat protein
22	33	70.2	680	2 T04647	hypothetical prote
23	33	70.2	712	2 ALBSG3	cyclomaltoextrin
24	33	70.2	713	1 ALBSG1	ATP-dependent DNA
25	33	70.2	792	2 A70476	chitinase VCA0027
26	33	70.2	849	2 D82510	hypothetical prote
27	32	68.1	256	2 B71264	ncp protein - Ent
28	32	68.1	328	1 E54392	glyceraldhyde-3-p
29	32	68.1	333	1 DEHGCT	

30	32	68.1	388	2 D72200	ornithine decarbox
31	32	68.1	454	2 PC4237	trans-cinnamate 4-
32	32	68.1	454	2 T37933	transcription acti
33	32	68.1	483	2 H81366	leucyl aminopeptid
34	32	68.1	503	2 T06522	trans-cinnamate 4-
35	32	68.1	505	2 JCS129	trans-cinnamate 4-
36	32	68.1	505	2 S68204	trans-cinnamate 4-
37	32	68.1	505	2 A47454	trans-cinnamate 4-
38	32	68.1	505	2 A84709	cinnamate-4-hydrox
39	32	68.1	505	2 T09525	trans-cinnamate 4-
40	32	68.1	505	2 JC1458	trans-cinnamate 4-
41	32	68.1	506	1 S36878	cytochrome P450 -
42	32	68.1	506	2 T14907	trans-cinnamate 4-
43	32	68.1	705	2 T34477	hypothetical prote
44	32	68.1	859	2 G86242	hypothetical prote
45	31.5	67.0	601	2 T26062	hypothetical prote

ALIGNMENTS

RESULT 1
A57396
PHAS-I protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 09-Jul-2004
C/Accession: A57396
R/Lin, T.A.; Kong, X.; Saltiel, A.R.; Blackshear, P.J.; Lawrence Jr., J.C.
J. Biol. Chem. 270, 18531-18538, 1995
A>Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, degradation, and
A/Reference number: A57396; MUID:95355483; PMID:7629182
A/Status: preliminary; not compared with conceptual translation
A/Accession: A57396
A/Molecule type: mRNA
A/Residues: 1-117 <LIN>
A/Cross-references: UNIPROT:Q60876; UNIPARC:UPI00000237BD; GB:U28656; NID:9881557; PIDN

Query Match 97.9%; Score 46; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
DB 50 RIYDRKFL 58

RESULT 2
A55258
Insulin-stimulated phosphoprotein PHAS-I - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55258; A54719
R/Lin, C.; Pang, S.; Kong, X.; Velleca, M.; Lawrence Jr., J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3730-3734, 1994
A>Title: Molecular cloning and tissue distribution of PHAS-I, an intracellular target for
A/Reference number: A55258; MUID:94224815; PMID:8170978
A/Accession: A55258
A/Molecule type: mRNA
A/Residues: 1-117 <HNA>
A/Cross-references: UNIPROT:Q62622; UNIPARC:UPI00000E729C; GB:U05014; NID:9468023; PIDN
R/Haystead, T.A.U.; Haystead, C.M.M.; Hu, C.; Lin, T.A.; Lawrence Jr., J.C.
J. Biol. Chem. 269, 23185-23191, 1994
A>Title: Phosphorylation of PHAS-I by mitogen-activated protein (MAP) kinase. Identific
A/Reference number: A54719; MUID:94365019; PMID:8083223
A/Accession: A54719
A/Molecule type: protein
A/Residues: 58-69 <HAY>
A/Cross-references: UNIPARC:UPI00001796E7
C/Keywords: phosphoprotein
F/64/Binding site: phosphate (Ser) (covalent) (by MAP kinase) #status experimental

Query Match 97.9%; Score 46; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.038;

C:Keywords: hydrolase; serine proteinase; transmembrane protein
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B96966
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85017
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: A85017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9M140; UNIPARC:UP100000A6604; GB:NC_001268; NID:g7267627; F
C:Genetics:
A:Gene: AT4G01300
A:Map position: 4

Query Match 74.5%; Score 35; DB 2; Length 1680;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRK 7
|||
Db 1601 RIYDRK 1607

RESULT 7

23BPL7
gene 3 protein - phage LP-7
C:Species: phage LP-7
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
C:Accession: J00531
R:Petri, J.B.; Schlegel, H.
Gene 88, 47-55, 1990
A:Title: Isolation of fragments with pac function for phage P22 from phage LP7 DNA and c
A:Reference number: P00093; MUID:90255967; PMID:2341038
A:Accession: J00531
A:Molecule type: DNA
A:Residues: 1-162 <PET>
A:Cross-references: UNIPARC:UP10000136B80; GB:M32403; NID:g215205; PIDN:AA88219.1; PID:
C:Comment: This protein is involved in the initiation of phage DNA packaging.
C:Genetics:
A:Gene: 3
A:Superfamily: phage P22 gene 3 protein
C:Keywords: DNA packaging

Query Match 72.3%; Score 34; DB 1; Length 162;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRK 8
:|||||
Db 101 QIYDQK 108

RESULT 8

A85017
hypothetical protein AT4G01300 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85017
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: A85017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9M140; UNIPARC:UP100000A6604; GB:NC_001268; NID:g7267627; F
C:Genetics:
A:Gene: AT4G01300
A:Map position: 4

Query Match 72.3%; Score 34; DB 2; Length 291;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
|||
Db 16 RIYTRKFL 24

RESULT 9

B96966
beta-mannanase ManB-like enzyme, contains Cnw-repeats [imported] - Clostridium acetobuty

C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B96966
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85017
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: A85017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9M140; UNIPARC:UP100000A6604; GB:NC_001268; NID:g7267627; F
C:Genetics:
A:Gene: AT4G01300
A:Map position: 4

Query Match 72.3%; Score 34; DB 2; Length 531;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 IYDRKF 8
:|||||
Db 224 LYDRKF 230

RESULT 10

T01714
hypothetical protein A IG002N01.4 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01714
R:Schect, P.; Magg, L.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002N01.
A:Reference number: Z14407
A:Accession: T01714
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1028 <SCH>
A:Cross-references: UNIPROT:O04604; UNIPARC:UP1000009F3CE; EMBL:AF007269; NID:g2191126;
C:Genetics:
A:Gene: ATSP_A_IG002N01.4
A:Introns: 78/2; 169/1; 234/3; 301/3; 387/3; 528/1; 974/1

Query Match 72.3%; Score 34; DB 2; Length 1028;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
|||
Db 45 RIYTRKFL 53

RESULT 11

B86194
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86194
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K...
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kilm, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sekano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86194
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-1251 <STO>
A:Cross-references: UNIPROT:Q9MA34, UNIPARC:UPI00000A4622, GB:AE005172, NID:g66850321, P1
C/Genetics:
A:Map position: 1

Query Match 72.3%; Score 34; DB 2; Length 1251;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKF 8
||:||||:
Db 949 RIYDKRF 956

RESULT 12
D90955
hypothetical protein Eca2612 [imported] - Escherichia coli (strain O157:H7, substrain R1
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: D90955
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hatfort, M.; Shinagawa, H.
DNA Reg. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <HAV>
A:Cross-references: UNIPROT:Q8XCD6, UNIPARC:UPI00000D4B0, GB:BA000007, PIDN:BA36035.1,
C/Genetics:
A:Experimental source: strain O157:H7, substrain R1MD 0509552
A:Gene: Eca2612
C/Superfamily: Escherichia coli hypothetical protein b1904

Query Match 70.2%; Score 33; DB 2; Length 107;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIYDRKF 9
||:||||:
Db 35 RLVDQAF 43

RESULT 13
A85804
hypothetical protein Z2959 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: A85804
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, B.U.; Davis, N.W.; Jim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85804
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <STO>
A:Cross-references: UNIPROT:Q8XCD6, UNIPARC:UPI00000D4B0, GB:AE005174, NID:g12515970, F
C/Genetics:
A:Experimental source: strain O157:H7, substrain EDL933
A:Gene: Z2959
C/Superfamily: Escherichia coli hypothetical protein b1904

Query Match 70.2%; Score 33; DB 2; Length 107;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIYDRKF 9
||:||||:
Db 35 RLVDQAF 43

RESULT 14
H64953
hypothetical protein b1904 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: H64953
R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64953
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <BAT>
A:Cross-references: UNIPROT:P76308, UNIPARC:UPI000013ABEC, GB:AE000284, GB:U00096, NID:g
A:Experimental source: strain K-12, substrain MG1655
C/Superfamily: Escherichia coli hypothetical protein b1904

Query Match 70.2%; Score 33; DB 2; Length 107;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIYDRKF 9
||:||||:
Db 35 RLVDQAF 43

RESULT 15
F69873
hypothetical protein ylbA - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: F69873
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumslein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69873
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-120 <KUN>
A:Cross-references: UNIPROT:Q34743, UNIPARC:UPI0000060363, GB:Z29111, GB:AL009126, NID:g
A:Experimental source: strain 168
C/Genetics:
A:Gene: ylbA
C/Superfamily: Bacillus subtilis hypothetical protein ylbA

Query Match 70.2%; Score 33; DB 2; Length 120;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIYDRKF 8
||:||||:
Db 38 RVIYDKF 45

Search completed: November 29, 2005, 23:02:33
Job time : 16.6818 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2005, 22:35:04 ; Search time 95.9091 Seconds
(without alignments)
73.562 Million cell updates/sec

Title: US-10-019-198A-3
Perfect score: 47
Sequence: 1 RIYDRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	97.9	93	2	Q4S362_TETNG
2	46	97.9	100	1	4EBP3_HUMAN
3	46	97.9	100	2	Q4RT85_TETNG
4	46	97.9	101	1	4EBP3_MOUSE
5	46	97.9	102	2	Q9B57_PIG
6	46	97.9	104	2	Q5U3D2_BRARE
7	46	97.9	112	1	4EBP_BRARE
8	46	97.9	112	2	Q4SL38_TETNG
9	46	97.9	113	2	Q6DJ11_XENLA
10	46	97.9	113	2	Q6NUG4_XENLA
11	46	97.9	113	2	Q6N12_BRARE
12	46	97.9	113	2	Q6P382_XENTR
13	46	97.9	116	1	4EBP1_MOUSE
14	46	97.9	116	1	4EBP1_RAT
15	46	97.9	117	1	4EBP1_HUMAN
16	46	97.9	120	1	4EBP2_HUMAN
17	46	97.9	120	1	4EBP2_MOUSE
18	46	97.9	120	2	Q6RG68_HUMAN
19	46	97.9	120	2	Q6PFS8_BRARE
20	42	89.4	376	2	Q7VJN8_HELP
21	37	78.7	333	2	Q4PB44_USTWA
22	37	78.7	679	2	Q6LH12_CAEBR
23	37	78.7	898	1	DPO1_BFR4
24	36	76.6	119	2	Q6SK07_BACIL
25	36	76.6	180	2	Q6LY06_METNP
26	36	76.6	296	2	Q98C65_RHIL0
27	36	76.6	298	2	Q6LWC8_CAEBR
28	36	76.6	367	2	Q89NS0_BRAJA
29	35	74.5	568	2	Q8V3R0_SWPV
30	35	74.5	114	2	Q56088_9BILA
31	35	74.5	122	2	Q7PN41_ANOGA

32	35	74.5	152	2	Q7W8P6_BORPA	Q7W8P6 bordetella
33	35	74.5	152	2	Q7W8B0_BORBR	Q7W8B0 bordetella
34	35	74.5	282	2	Q50L77_ENTHI	Q50L77 entamoeba h
35	35	74.5	364	2	Q609W2_METCA	Q609W2 methylococc
36	35	74.5	867	2	Q4RLD0_TETNG	Q4RLD0 tetradon n
37	35	74.5	913	2	Q6JKD2_SNUCL	Q6JKD2 neodipiron
38	35	74.5	1061	2	Q5B110_DROME	Q5B110 drosophila
39	35	74.5	1679	1	FUR2_DROME	P30432 drosophila
40	34	72.3	54	2	Q91LJ0_MSSV	Q91LJ0 white spot
41	34	72.3	119	2	Q5L106_GEOXA	Q5L106 geobacillus
42	34	72.3	120	2	Q5D171_SCHJA	Q5D171 schistosoma
43	34	72.3	162	1	TERM_BPLP7	P16937 bacterioph
44	34	72.3	162	1	Q80250_BPPS3	Q80250 bacterioph
45	34	72.3	162	2	Q80321_BPPS1	Q80321 bacterioph

ALIGNMENTS

```
RESULT 1
Q4S362_TETNG PRELIMINARY; PRT; 93 AA.
ID Q4S362:
AC Q4S362:
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 4 SCAP14752, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00024778001;
GN Tetradon nigroviridis (Green puffer).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozou-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bieumont C., Skallit Z., Catroico L., Poulin J., De Bernardis V.,
RA Crnaud C., Duprat S., Broctier P., Coucanceau D.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RA Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014752; CACG04920.1; -; Genomic_DNA.
FT NON-TER 93
SQ SEQUENCE 93 AA; 1009 MW; 9329D93EA4C30996 CRC64;
Query Match 97.9%; Score 46; DB 2; Length 93;
Best local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

4EBP3 HUMAN
ID 4EBP3 HUMAN STANDARD; PRT; 100 AA.
AC O60516
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Eukaryotic translation initiation factor 4E-binding protein 3 (4E-BP3)
GN (EIF4E-binding protein 3).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RX LEU-45, AND TISSUE SPECIFICITY.
RX MEDLINE=98256334; PubMed=9593750; DOI=10.1074/jbc.273.22.14002;
RA Poulin F., Gingras A.-C., Olsen H., Chevalier S., Sonenberg N.;
RT "4E-BP3, a new member of the eukaryotic initiation factor 4E-binding
RT protein family.";
RL J. Biol. Chem. 273:14002-14007(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lymph;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrini P., Prange C.J.,
RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Regulates eIF4E activity by preventing its assembly into
CC the eIF4F complex.
CC -1- SUBUNIT: EIF4EBP3 interacts with EIF4E.
CC -1- TISSUE SPECIFICITY: Expression is highest in skeletal muscle,
CC heart, kidney, and pancreas, whereas there is very little
CC expression in brain and thymus.
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: Belongs to the eIF4E-binding protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF038869; AAC39761.1; -; mRNA.
DR EMBL; BC010881; AAH10881.1; -; mRNA.
DR EMBL; BC069293; AAH69293.1; -; mRNA.
DR EMBL; BC073751; AAH73751.1; -; mRNA.
DR EMBL; ENSG000000131503; Homo sapiens.
DR HGNC; HGNC:3290; EIF4EBP3.
DR MIM; 603483; -;
DR GO; GO:0016281; C:eukaryotic translation initiation factor 4F. .; NAS.
DR GO; GO:0030371; F:translation repressor activity; NAS.
DR GO; GO:0045947; P:negative regulation of translational initia. .; NAS.
DR InterPro; IPR006066; EIF4EBP.
DR PANTHER; PTHR12669; EIF4EBP; 1.

DR Pfam; PF05456; eIF_4EBP; 1.
KW Phosphorylation; Protein synthesis inhibitor; Translation regulation.
FT MUTAGEN 40 Y->A: Loss of interaction with EIF4E.
FT MUTAGEN 45 L->A: Loss of interaction with EIF4E.
SQ SEQUENCE 100 AA; 10873 MW; FD29A7F3829E546E CRC64;
Query Match 97.9%; Score 46; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIYDRKFL 9
Db 37 RIYDRKFL 45
RESULT 3
Q4RT89_TETNG
ID Q4RT89_TETNG PRELIMINARY; PRT; 100 AA.
AC Q4RT89;
DT 13-SEP-2005 (TREMURel. 31, Created)
DT 13-SEP-2005 (TREMURel. 31, Last sequence update)
DT 13-SEP-2005 (TREMURel. 31, Last annotation update)
DE Chromosome 1 SCAF14998, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0029360001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Uallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Maucell S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castellani V., Katinka M., Vachette B.,
RA Blemont C., Skalli Z., Carroccio L., Poulat J., De Bernardis V.,
RA Craud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Kella G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Pellerin M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollis H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB0104998; CAG08393.1; -; genomic_DNA.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 10943 MW; A1BAE31ACFD59873 CRC64;
Query Match 97.9%; Score 46; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIYDRKFL 9
Db 47 RIYDRKFL 55
RESULT 4
4EBP3_MOUSE
ID 4EBP3_MOUSE STANDARD; PRT; 101 AA.
AC O80VV3;
DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Eukaryotic translation initiation factor 4E-binding protein 3 (4E-BP3)
 DE (eIF4E-binding protein 3).
 GN Name=eIF4ebp3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Poulin F., Sonenberg N.;
 RT "Two overlapping reading frames in the second exon of the
 RL translational inhibitor 4E-BP3."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Testis;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnaa.242603699;
 RA Strauberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohshiyuki S., Carrinot P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosnak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
 RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Regulates eIF4E activity by preventing its assembly into
 CC the eIF4 complex (By similarity).
 CC -!- SUBUNIT: eIF4EBP3 interacts with eIF4E (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- SIMILARITY: Belongs to the eIF4E-binding protein family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, AY226182; AA073448.1; -, mRNA.
 DR EMBL, BC061242; AA061242.1; -, mRNA.
 DR Ensembl, ENSMUSG00000033775; Mus musculus.
 DR MGI, MGI:1270847; EIf4ebp3.
 DR InterPro, IPR008606; EIf4EBP.
 DR PANTHER, PTHR12669; EIf4EBP, 1
 DR PhosphoSitePlus, Protein synthesis inhibitor; Translation regulation.
 SQ SEQUENCE 101 AA; 11019 MW; 78F82052696ABD7 CRC64;

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Query Match          97.9%; Score 46; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches      9; Conservative      0; Indels      0; Gaps      0;

QY      1 RIYDRKFL 9
        |||||
Db      37 RIYDRKFL 45

RESULT 5
Q9BG57_FIG

```

ID	O9BG57.PIG	PRELIMINARY;	PRF:	102 AA.
AC	O9BG57;			
DT	01-JUN-2001	(TREMBlrel_17,	Created)	
DT	01-JUN-2001	(TREMBlrel_17,	Last sequence update)	
DT	01-MAR-2004	(TREMBlrel_26,	Last annotation update)	
DE	Translation initiation factor 4B binding protein 1 (Fragment).			
OS	Sus scrofa	(Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;			
CC	Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RA	NUCLEOTIDE SEQUENCE.			
RP	Anger M., Klima J., Kubelka M., Carnwath J.W., Niemann H.;			
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AF373389; AAK08101.1; -; mRNA.			
DR	GO; GO:0008180; P:eukaryotic translation initiation factor 4E binding; IEA.			
DR	GO; GO:0003743; P:translation initiation factor activity; IEA.			
DR	GO; GO:0045947; P:negative regulation of translational initia. . . ; IEA.			
DR	InterPro; IPR008606; EIF4BP.			
DR	Pfam; PF05456; eIF_4EBP; 1.			
KW	Initiation factor.			
FT	NON TER	1		
FT	NON TER	102		
SEQ	SEQUENCE	102 AA;	10697 MW;	01C8B769D02658E9 CRC64;
QY	Query Match	97.9%;	Score 46;	DB 2; Length 102;
	Best Local Similarity	100.0%;	Pred. NO. 0.17;	
	Matches 9;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0.
DB	1 RIHYDKFL 9 41 RIHYDKFL 49			

ID	OSU3D2_BRAPE	PRT	104 AA.
AC	OSU3D2_0503D2_01-FEB-2005 (TREMBlrel. 29, Created)		
DT	01-FEB-2005 (TREMBlrel. 29, Last sequence update)		
DT	01-FEB-2005 (TREMBlrel. 29, Last annotation update)		
DE	ZGC:103720.		
GN	ORFNames=zgc:103720;		
OS	Brachydanio rerio (zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Liver;		
RX	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Sheman C.M., Schuler G.D.,		
RA	Altchul S.F., Zeeberg B., Buecor K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditcheiko L., Martinsina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., Mewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	White J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,		
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Director MGC Project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC085595; AAH85595.1; -, mRNA.
DR ZFIN; ZDB-GENE-04114-44; zgc:103720.
DR GO; GO:0008190; P:eukaryotic initiation factor 4E binding; IEA.
DR GO; GO:0045947; P:negative regulation of translational initia. . .; IEA.
DR InterPro; IPR008606; EIF4EBP.
DR Pfam; PF05456; eIF_4EBP.1.
SQ SEQUENCE 104 AA; 11427 MW; 446FD0D99AEFB750 CRC64;

Query Match 97.9%; Score 46; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
Db 46 RIYDRKFL 54

RESULT 7
4EBP_BRARE STANDARD; PRT; 112 AA.
ID 4EBP_BRARE
AC 098TT6;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Eukaryotic translation initiation factor 4E-1A-binding protein (eIF4E-1A-binding protein) (4E-BP).
GN ORFNames=zgc:56330;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND INTERACTION WITH EIF4E1A.
RX PubMed:14701818; DOI=10.1074/jbc.M31688200;
RA Robalino J., Joshi B., Fahrnkruug S.C., Jagus R.;
RA "Two zebrafish eIF4E family members are differentially expressed and functionally divergent.";
RT functionally divergent.";
RL J. Biol. Chem. 279:10532-10541(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Regulates eif4e1a activity by preventing its assembly into the eIF4F complex (By similarity).
CC -1- SUBUNIT: Interacts with eif4e1a.
CC -1- SIMILARITY: Belongs to the eIF4E-binding protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; AF332983; AAC50053.1; -, mRNA.
DR EMBL; BC046079; AAH46079.1; -, mRNA.
DR Ensemble; ENSDARG00000023315; Danio rerio.
DR ZFIN; ZDB-GENE-030131-3211; zgc:56330.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0030371; F:translation repressor activity; ISS.
DR GO; GO:0045947; P:negative regulation of translational initia. . .; ISS.
DR InterPro; IPR008606; EIF4EBP.
DR PANTHER; PTHR12669; EIF4EBP.1.
DR Pfam; PF05456; eIF_4EBP.1.
DR KEGG; K04480; eIF4E; Translation regulation.
SQ SEQUENCE 112 AA; 12531 MW; F71BEA295722826E CRC64;

Query Match 97.9%; Score 46; DB 1; Length 112;
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
Db 47 RIYDRKFL 55

RESULT 8
Q4SL38_TETNG PRELIMINARY; PRT; 112 AA.
ID Q4SL38_TETNG
AC Q4SL38;
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome 17 SCAP14563, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00016435001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
OC Acanthomorphia; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cartolico L., Poulain J., De Berardinis V.,
RA Ceraud C., Duprat S., Brottier P., Couranceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McKernan P., Bosak S.,
RA Kellis M., Wolf J.M., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope: Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL; CAAB0104563; CAF98644.1; -, Genomic_DNA.
FT NON TER 112
SQ SEQUENCE 112 AA; 12465 MW; A158734EB80064E1 CRC64;

Query Match 97.9%; Score 46; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIYDRKFL 9
Db 45 RIYDRKFL 53

RESULT 9
Q6DJ11_XENLA PRELIMINARY; PRT; 113 AA.
ID Q6DJ11_XENLA
AC Q6DJ11;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MG83416 protein.
DE MG83416 protein.
GN Name=MG83416;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
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RA Diatchenko L., Soares M.B., Bonaldo M.F., Caezant T.L., Scheetz T.E.,
RA Stjepic M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bork S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065546; AAH65546.1; -; mRNA.
DR ZFIN; ZDB-GENE-011118-83; elf4ebp2.
DR GO; GO:0008190; F:euukaryotic initiation factor 4E binding; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0045947; P:negative regulation of translational initia. . .; IEA.
DR InterPro; IPR008606; EIF4EBP.
DR Pfam; PF05456; eIF_4EBP; 1.
DR Initiation factor.
KM SEQUENCE 113 AA; 12441 MW; 122CG91F3AFVEFF9 CRC64;
SQ
Query Match 97.9%; Score 46; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RIYDRKFL 9
Db 47 RIYDRKFL 55
RESULT 12
Q6P382_XENTR PRELIMINARY; PRT; 113 AA.
ID Q6P382_XENTR PRELIMINARY; PRT; 113 AA.
AC Q6P382;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75579.
GN Name=MGC75579;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
CX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.2426038959;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
RA Rana S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bork S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064150; AAH64150.1; -; mRNA.
DR GO; GO:0008190; F:euukaryotic initiation factor 4E binding; IEA.
DR GO; GO:0045947; P:negative regulation of translational initia. . .; IEA.
DR InterPro; IPR008606; EIF4EBP.
DR Pfam; PF05456; eIF_4EBP; 1.
DR Hypothetical protein.
KM SEQUENCE 113 AA; 12361 MW; 060A30F0D1361A CRC64;
SQ
Query Match 97.9%; Score 46; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RIYDRKFL 9
Db 47 RIYDRKFL 55
RESULT 13
4EBPL_MOUSE STANDARD; PRT; 116 AA.
ID 4EBPL_MOUSE STANDARD; PRT; 116 AA.
AC Q60876; Q9CZ40;
DT 10-OCT-2003 (Ref. 42, Created)
DT 13-SEP-2005 (Ref. 48, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
DE Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1)
DE (eIF4E-binding protein 1) (Phosphorylated heat- and acid-stable
DE protein regulated by insulin 1) (PHAS-I).
GN Name=eIF4ebp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY,
RP PHOSPHORYLATION, AND INTERACTION WITH EIF4E.
RA MEDLINE=5535483; PubMed=7629182; DOI=10.1074/jbc.270.31.18531;
RX Lin T.-A., Kong X., Sattler A.R., Blackshear P.J., Lawrence J.C. Jr.,
RT "Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis,
RT degradation, and phosphorylation by a rapamycin-sensitive and mitogen-
RT activated protein kinase-independent pathway.";
RL J. Biol. Chem. 270:18531-18538(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1098/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schmitt L.M., Kamplin A., Matsuda H., Batolov S., Betsel K.W.,
RA Blake J.B., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dregani T.A., Fletcher C.F., Forrest A., Frazar K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Girimond S., Gutrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji K., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanyaga A., Kurouchkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

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RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imocani K., Ichii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shingawa A.,
 RA Yasunishi E., Yoshino M., Waterson R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6; TISSUE=Mammary gland;
 RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Teshiguchi S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gricham J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallegange D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Regulates eIF4E activity by preventing its assembly into
 CC the eIF4F complex. Mediates the regulation of protein translation
 CC by hormones, growth factors and other stimuli that signal through
 CC the MAP kinase pathway.
 CC -1- SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 to
 CC interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and
 CC MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the
 CC complex allowing EIF4G1/EIF4G3 to bind and consequent initiation
 CC of translation. Rapamycin can attenuate insulin stimulation,
 CC mediated by FRKBP.
 CC TISSUE SPECIFICITY: Highest expression in fat cells.
 CC -1- PTM: Phosphorylated on serine and threonine residues in response
 CC to insulin, EGF and PDGF.
 CC -1- SIMILARITY: Belongs to the eIF4E-binding protein family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL: U28656; AAA86818.1; -, mRNA.
 DR EMBL: AK013033; BAB28612.1; -, mRNA.
 DR EMBL: BC002045; AAH02045.1; -, mRNA.
 DR PIR: A57396; A57396.
 DR Ensemble: ENSEMBL:000000031490; Mus musculus.
 DR MGI: MGI:103267; B144ebp1.
 DR GO: GO:0005151; F:protein binding; IPI.
 DR GO: GO:0003071; F:translation repressor activity; TAS.
 DR GO: GO:0008286; P:insulin receptor signaling pathway; IDA.
 DR GO: GO:0006446; P:regulation of translational initiation; TAS.
 DR InterPro: IPR008606; EIF4EBP.
 DR PANTHER: PTHR12669; EIF4EBP; 1.
 DR Pfam: PF05456; eIF_4EBP; 1.
 DR Acetylation; phosphorylation; Protein synthesis inhibitor;
 KW translation regulation.
 FT INIT_MET 0 By similarity.

FT MOD_RES 1 1 N-acetylserine (By similarity).
 FT MOD_RES 63 63 Phosphoserine (by MAPK1 and MAPK3) (By
 FT CONFLICT 92 92 similarity).
 FT CONFLICT 92 92 S->N (in Ref. 2).
 SQ SEQUENCE 116 AA; 12194 MM; C458968404C4C87 CRC64;
 Query Match 97.9%; Score 46; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. NO. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RIYDRKPL 9
 Db 49 RIYDRKPL 57
 ID 4EBP1 RAT STANDARD; PRT; 116 AA.
 AC Q62622;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1)
 DE (eIF4E-binding protein 1) (Phosphorylated heat- and acid-stable
 DE protein regulated by insulin 1) (PHAS-I).
 GN Name=EIF4ebp1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 17-32; 42-52; 61-79
 RP AND 97-116, PHOSPHORYLATION, AND TISSUE SPECIFICITY.
 RP STRAIN=Sprague-Dawley; TISSUE=adipocyte, and skeletal muscle;
 RX MEDLINE=94224815; PubMed=8170978;
 RA Hu C., Pang S., Kong X., Vellica M., Lawrence J.C., Jr.;
 RT "Molecular cloning and tissue distribution of PHAS-I, an intracellular
 RT target for insulin and growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3730-3734(1994).
 RN [2]
 RP FUNCTION: INTERACTION WITH EIF4E, PHOSPHORYLATION OF SER-63 BY MAPK1
 RP AND MAPK3, AND MUTAGENESIS OF SER-63.
 RX MEDLINE=95025978; PubMed=7939721;
 RA Lin T.-A., Kong X., Haystead T.A.U., Pause A., Belsham G.J.,
 RA Sonenberg N., Lawrence J.C., Jr.;
 RT "PHAS-I as a link between mitogen-activated protein kinase and
 RT translation initiation.";
 RL Science 265:653-656(1994).
 CC -1- FUNCTION: Regulates eIF4E activity by preventing its assembly into
 CC the eIF4F complex. Mediates the regulation of protein translation
 CC by hormones, growth factors and other stimuli that signal through
 CC the MAP kinase pathway.
 CC -1- SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 to
 CC interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and
 CC MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the
 CC complex allowing EIF4G to bind and consequent initiation of
 CC translation. Rapamycin can attenuate insulin stimulation, mediated
 CC by FRKBP.
 CC TISSUE SPECIFICITY: Expressed in all tissues examined; highest
 CC levels in fat and skeletal tissue, lowest levels in kidney.
 CC -1- PTM: Phosphorylated on serine and threonine residues in response
 CC to insulin, EGF and PDGF.
 CC -1- SIMILARITY: Belongs to the eIF4E-binding protein family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL: U05014; AAA66938.1; -, mRNA.
 DR PIR: A55258; A55258.

DR Ensembl; ENSRNOG00000012582; Rattus norvegicus.
DR RGD; 620259; Eif4ebp1.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0008286; P:insulin receptor signalling pathway; IDA.
DR InterPro; IPR008606; EIF4EBP.
DR PANTHER; PTHR12669; EIF4EBP; 1.
DR Pfam; PF05456; eif4ebp; 1.
DR Acetylation; Direct protein sequencing; Phosphorylation;
KW Protein synthesis inhibitor; Translation regulation.
KM Protein synthesis inhibitor; Translation regulation.
FT INT_MET 0 0
FT MOD_RES 1 1 N-acetylsertine (By similarity).
FT MOD_RES 63 63 Phosphoserine (by MAPK1 and MAPK3).
FT MUTAGEN 63 63 S->A: Decreases phosphorylation by MAPK1
FT and MAPK3.
FT CONFLICT 18 18 R->N (in Ref. 1; AA sequence).
FT CONFLICT 68 68 T->P (in Ref. 1; AA sequence).
FT CONFLICT 74 74 P->L (in Ref. 1; AA sequence).
SQ SEQUENCE 116 AA; 12273 MW; C449987B3DDFE877 CRC64;
Query March 97.9%; Score 46; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. NO. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIYDRKFL 9
Db 49 RIYDRKFL 57
RESULT 15
4EBP1 HUMAN STANDARD; PRT; 117 AA.
ID 4EBP1 HUMAN
AC Q13541; O61BN3;
DT 10-OCT-2003 (Ref. 42, Created)
DT 13-SEP-2005 (Ref. 48, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
DE Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1)
DE (eif4E-binding protein 1) (Phosphorylated heat- and acid-stable
DE protein regulated by insulin 1) (PHAS-1).
GN Name=EIF4EBP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, INTERACTION WITH EIF4E, AND
RP PHOSPHORYLATION.
RC TISSUE=Placenta;
RX MEDLINE=95021760; PubMed=7935836; DOI=10.1038/371762a0;
RA Pause A., Belsham G.J., Gingras A.-C., Donze O., Lin T.-A.,
RA Lawrence J.C. Jr., Sonenberg N.,
RT "Insulin-dependent stimulation of protein synthesis by phosphorylation
RT of a regulator of 5'-cap function.";
RT Nature 371:762-767(1994).
RL [2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP Ito M., Shichijo S., Tsuda N., Ochi M., Harashima N., Saito N.,
RA Itoh K.;
RT "Identification of multiple genes and immunogenic epitopes of
RT pancreatic cancer cells.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry

RT vector (pDONR201)." to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon, and Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquailano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE OF 1-12, AND ACETYLATION SITE SER-1.
RC TISSUE=Platelet;
RX MEDLINE=22608296; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goetghals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekekerkhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
RN [7]
RP INTERACTIONS WITH EIF4E AND EIF4G.
RX MEDLINE=96091142; PubMed=8521827;
RA Haghighat A., Mader S., Pause A., Sonenberg N.;
RT "Repression of cap-dependent translation by 4E-binding protein 1:
RT competition with p20 for binding to eukaryotic initiation factor-
RT 4E.";
RL EMBO J. 14:5701-5709(1995).
CC -1- FUNCTION: Regulates EIF4E activity by preventing its assembly into
CC the eIF4 complex. Mediates the regulation of protein translation
CC by hormones, growth factors and other stimuli that signal through
CC the MAP kinase pathway.
CC -1- SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 to
CC interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and
CC MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the
CC complex allowing EIF4G1/EIF4G3 to bind and consequent initiation
CC of translation. Rapamycin can attenuate insulin stimulation.
CC mediated by FKBP5.
CC -1- INTERACTION:
CC P06730:EIF4E; NbExp=2; InAc=EBI-74090, EBI-73440;
CC O60573:EIF4E3; NbExp=1; InAc=EBI-74090, EBI-398610;
CC -1- PTM: Phosphorylated on serine and threonine residues in response
CC to insulin, EGF and PDGF.
CC -1- SIMILARITY: Belongs to the eIF4E-binding protein family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; L36055; AAA62269.1; -; mRNA.
DR EMBL; AB044548; BA818650.1; -; mRNA.
DR EMBL; BT007162; AAR35826.1; -; mRNA.
DR EMBL; CR456769; CAG33050.1; -; mRNA.
DR EMBL; BC004459; AA804459.1; -; mRNA.
DR EMBL; BC058073; AAH58073.1; -; mRNA.
DR PIR; S50866; S50866.

DR InAct; Q13541; -.
 DR Ensembl; ENSG00000187840; Homo sapiens.
 DR HGNC; HGNC:3288; EIF4EBP1.
 DR Reactome; Q13541; -.
 DR MIT; 602223; -.
 DR GO; GO:0006445; P:regulation of translation; TAS.
 DR InterPro; IPR008606; EIF4EBP.
 DR PANTHER; PTHR12669; EIF4EBP; 1.
 DR Pfam; PF05456; eIF_4EBP; 1.
 KW Acetylation; Direct protein sequencing; Phosphorylation;
 KW Protein synthesis inhibitor; Translation regulation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 N-acetyls erine
 FT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By
 similarity)
 SQ SEQUENCE 117 AA; 12449 MM; 4682ACF774270D8D CRC64;
 QY 1 RIYDRKFL 9
 DB 50 RIYDRKFL 58
 Query Match 97.9%; Score 46; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 29, 2005, 23:01:22
 Job time : 98.9091 secs

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OM protein - protein search, using BW model

Run on: November 29, 2005, 22:45:04 ; Search time 23.8636 Seconds
(without alignments)
34.645 Million cell updates/sec

Title: US-10-019-198A-3
Perfect score: 47
Sequence: 1 RIYDRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	97.9	100	1	US-08-869-733-1
2	46	97.9	100	2	US-09-215-063-1
3	46	97.9	100	2	US-10-096-703-1
4	46	97.9	118	2	US-09-949-016-7744
5	46	97.9	120	1	US-08-869-733-3
6	46	97.9	120	1	US-08-869-733-4
7	46	97.9	120	2	US-09-215-063-3
8	46	97.9	120	2	US-09-215-063-4
9	46	97.9	120	2	US-10-096-703-3
10	46	97.9	120	2	US-10-096-703-4
11	46	97.9	120	2	US-09-949-016-7860
12	37	78.7	898	1	US-08-465-995A-2
13	37	78.7	898	1	US-08-465-995A-4
14	37	78.7	898	1	US-08-465-994C-2
15	37	78.7	898	1	US-08-465-994C-4
16	37	78.7	898	1	US-08-966-145-2
17	37	78.7	898	1	US-08-966-145-4
18	37	78.7	898	1	US-08-101-593-2
19	37	78.7	898	1	US-08-101-593-4
20	36	76.6	341	2	US-09-107-532A-3743
21	33	70.2	193	2	US-09-540-236-2196
22	33	70.2	315	2	US-09-902-540-14851
23	33	70.2	345	2	US-09-134-000C-5685
24	33	70.2	358	2	US-09-352-991A-24894
25	33	70.2	375	2	US-09-489-039A-10175
26	33	70.2	685	2	US-08-947-965-72
27	33	70.2	686	2	US-08-947-965-73

28	32	68.1	61	2	US-09-540-236-2324	Sequence 2324, Ap
29	32	68.1	143	2	US-09-270-767-35637	Sequence 35637, A
30	32	68.1	143	2	US-09-270-767-50854	Sequence 50854, A
31	32	68.1	361	2	US-09-854-122-43	Sequence 42, Appl
32	32	68.1	362	2	US-09-854-122-42	Sequence 42, Appl
33	32	68.1	394	2	US-09-248-796A-20723	Sequence 20723, A
34	32	68.1	501	2	US-09-158-767-15	Sequence 15, Appl
35	32	68.1	501	2	US-09-158-767-16	Sequence 15, Appl
36	32	68.1	501	2	US-09-158-767-17	Sequence 15, Appl
37	32	68.1	501	2	US-09-158-767-18	Sequence 15, Appl
38	32	68.1	501	2	US-09-713-794-15	Sequence 16, Appl
39	32	68.1	501	2	US-09-713-794-16	Sequence 16, Appl
40	32	68.1	501	2	US-09-713-794-17	Sequence 16, Appl
41	32	68.1	501	2	US-09-713-794-18	Sequence 16, Appl
42	32	68.1	505	2	US-09-627-216A-12	Sequence 12, Appl
43	32	68.1	505	2	US-09-126-420A-22	Sequence 22, Appl
44	32	68.1	505	2	US-09-765-873A-12	Sequence 12, Appl
45	32	68.1	519	2	US-09-854-122-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-869-733-1
Sequence 1, Application US/08869733
Patent No. 5955278
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BSTANOT01
CLONE: 805296
US-08-869-733-1

Query Match 97.9%
Best Local Similarity 100.0%
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
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Db 37 RIYDRKFL 45

RESULT 2

US-09-215-063-1
; Sequence 1, Application US/09215063
; Patent No. 6365714
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215.063
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/869,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BSTMN0T01
; CLONE: 805296
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-215-063-1
Query Match 97.9%; Score 46; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
|||
Db 37 RIYDRKFL 45

RESULT 3

US-10-096-703-1
; Sequence 1, Application US/10096703
; Patent No. 6677126
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BSTMN0T01
CLONE: 805296
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-096-703-1

Query Match 97.9%; Score 46; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIYDRKFL 9
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Db 37 RIYDRKFL 45

RESULT 4

US-09-949-016-7744
; Sequence 7744, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7744
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7744
Query Match 97.9%; Score 46; DB 2; Length 118;

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 5
US-08-869-733-3

/ Sequence 3, Application US/08869733
/ Patent No. 5955278
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Hawkins, Phillip R.
/ TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/869,733
/ FILING DATE: Herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0310 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 561632
/ US-08-869-733-3

Query Match 97.9%; Score 46; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 6
US-08-869-733-4
/ Sequence 4, Application US/08869733
/ Patent No. 5955278
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Hawkins, Phillip R.
/ TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
/ NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/869,733
/ FILING DATE: Herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0310 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
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/ LIBRARY: GenBank
/ CLONE: 1658516
/ US-08-869-733-4

Query Match 97.9%; Score 46; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 7
US-09-215-063-3
/ Sequence 3, Application US/09215063
/ Patent No. 6365714
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Hawkins, Phillip R.
/ TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/215,063
/ FILING DATE: 17-Dec-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/869,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 561632
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-215-063-3

Query Match          97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 8
US-09-215-063-4
; Sequence 4, Application US/09215063
; Patent No. 6365714
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,063
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/869,733
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 561632
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-096-703-3

Query Match          97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 10
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; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1658516
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-215-063-4

Query Match          97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 9
US-10-096-703-3
; Sequence 3, Application US/10096703
; Patent No. 6677126
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,703
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/215,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 561632
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-096-703-3

Query Match          97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 10
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US-10-096-703-4
; Sequence 4, Application US/10096703
; Patent No. 6677126
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PASTESEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,703
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/215,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 1658516
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-096-703-4

Query Match 97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
DB 51 RIYDRKFL 59

RESULT 11
US-09-949-016-7860
; Sequence 7860, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO: 7860
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7860

Query Match 97.9%; Score 46; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
DB 51 RIYDRKFL 59

RESULT 12
US-08-465-995A-2
; Sequence 2, Application US/08465995A
; Patent No. 5660980
; GENERAL INFORMATION:
; APPLICANT: Myron F. Goodman
; APPLICANT: Linda J. Reha-Krantz
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING
; VARIANT T4 POLYMERASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Robbins, Berliner & Carson, LLP
; STREET: 201 No. 5660980th Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: ASCII DOS/TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,995A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert Berliner
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 1920-305D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/977-1001
; TELEFAX: 213/977-1003
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-995A-2

Query Match 78.7%; Score 37; DB 1; Length 898;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYDRKFL 9
DB 99 IYDRKFL 106

RESULT 13
US-08-465-995A-4
; Sequence 4, Application US/08465995A
; Patent No. 5660980
; GENERAL INFORMATION:
; APPLICANT: Myron F. Goodman
; APPLICANT: Linda J. Reha-Krantz

;/ TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING
;/ TITLE OF INVENTION: VARIANT T4 POLYMERASES
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESSES:
;/ ADDRESS: Robbins, Berliner & Carson, LLP
;/ STREET: 201 No. 5660980th Figueroa Street, Suite 500
;/ CITY: Los Angeles
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 90012-2628
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: floppy disk
;/ OPERATING SYSTEM: ASCII DOS/TEXT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/465,995A
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Robert Berliner
;/ REGISTRATION NUMBER: 20,121
;/ REFERENCE/DOCKET NUMBER: 1920-305D2
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 213/977-1001
;/ TELEFAX: 213/977-1003
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 898 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-465-995A-4

Query Match 78.7%; Score 37; DB 1; Length 898;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IIVDRKFL 9
|:|||||:
Db 99 IIVDRKFLV 106

RESULT 14
US-08-465-994C-2
;/ Sequence 2, Application US/08465994C
;/ Patent No. 5928919
;/ GENERAL INFORMATION:
;/ APPLICANT: MYRON F. GOODMAN
;/ APPLICANT: LINDA L. REHA-KRANTZ
;/ TITLE OF INVENTION: VARIANT DNA POLYMERASES
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESSES:
;/ ADDRESS: Robbins, Berliner & Carson, LLP
;/ STREET: 201 No. 5928919th Figueroa Street, Suite 500
;/ CITY: Los Angeles
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 90012-2628
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: floppy disk
;/ OPERATING SYSTEM: ASCII DOS/TEXT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/465,994C
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MARGARET A. CHURCHILL
;/ REGISTRATION NUMBER: 39,944
;/ REFERENCE/DOCKET NUMBER: 1920-305D1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 213/977-1001
;/ TELEFAX: 213/977-1003

;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 898 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-465-994C-2

Query Match 78.7%; Score 37; DB 1; Length 898;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IIVDRKFL 9
|:|||||:
Db 99 IIVDRKFLV 106

RESULT 15
US-08-465-994C-4
;/ Sequence 4, Application US/08465994C
;/ Patent No. 5928919
;/ GENERAL INFORMATION:
;/ APPLICANT: MYRON F. GOODMAN
;/ APPLICANT: LINDA L. REHA-KRANTZ
;/ TITLE OF INVENTION: VARIANT DNA POLYMERASES
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESSES:
;/ ADDRESS: Robbins, Berliner & Carson, LLP
;/ STREET: 201 No. 5928919th Figueroa Street, Suite 500
;/ CITY: Los Angeles
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 90012-2628
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: floppy disk
;/ OPERATING SYSTEM: ASCII DOS/TEXT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/465,994C
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MARGARET A. CHURCHILL
;/ REGISTRATION NUMBER: 39,944
;/ REFERENCE/DOCKET NUMBER: 1920-305D1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 213/977-1001
;/ TELEFAX: 213/977-1003
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 898 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-465-994C-4

Query Match 78.7%; Score 37; DB 1; Length 898;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IIVDRKFL 9
|:|||||:
Db 99 IIVDRKFLV 106

Search completed: November 29, 2005, 23:04:22
Job time : 24.8636 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: November 29, 2005, 22:52:34 ; Search time 77.9545 Seconds
(without alignments)
53.599 Million cell updates/sec

Title: US-10-019-198a-3
Perfect score: 47
Sequence: 1 RIYDRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	97.9	9	4	US-10-353-929-14
2	46	97.9	16	3	US-09-973-473-6
3	46	97.9	16	3	US-09-973-473-7
4	46	97.9	16	3	US-09-973-473-8
5	46	97.9	100	4	US-10-096-703-1
6	46	97.9	100	4	US-10-096-703-1
7	46	97.9	117	5	US-10-631-467-1617
8	46	97.9	118	4	US-10-353-929-48
9	46	97.9	118	5	US-10-631-467-917
10	46	97.9	119	3	US-09-925-300-1267
11	46	97.9	120	4	US-10-096-703-3
12	46	97.9	120	4	US-10-096-703-4
13	46	97.9	138	3	US-09-925-301-1164
14	42	89.4	63	4	US-10-425-115-251396
15	41	87.2	9	4	US-10-353-929-15
16	39	83.0	16	3	US-09-973-473-15
17	38	80.9	128	4	US-10-210-281-68
18	37	78.7	898	4	US-10-401-403-197
19	35	74.5	105	4	US-10-425-115-272454
20	35	74.5	977	4	US-10-425-115-272448
21	35	74.5	1679	6	US-11-097-143-8286
22	34	72.3	16	3	US-09-973-473-16
23	34	72.3	16	3	US-09-973-473-17
24	34	72.3	223	6	US-11-097-143-24573
25	34	72.3	484	4	US-10-425-114-49505
26	34	72.3	500	4	US-10-425-115-261205
27	34	72.3	500	4	US-10-425-115-261205

ALIGNMENTS

28	34	72.3	601	5	US-10-732-923-16954	Sequence 16954, A
29	34	72.3	728	4	US-10-424-599-189465	Sequence 189465, A
30	34	72.3	790	4	US-10-437-963-187691	Sequence 187691, A
31	34	72.3	1066	4	US-10-437-963-187680	Sequence 187680, A
32	33	70.2	69	4	US-10-425-115-185633	Sequence 185633, A
33	33	70.2	99	4	US-10-424-599-175084	Sequence 175084, A
34	33	70.2	107	4	US-10-282-122A-42947	Sequence 42947, A
35	33	70.2	128	4	US-10-767-701-15373	Sequence 35373, A
36	33	70.2	150	4	US-10-425-115-364879	Sequence 364879, A
37	33	70.2	173	4	US-10-767-701-48906	Sequence 48906, A
38	33	70.2	344	4	US-10-282-122A-66350	Sequence 66350, A
39	33	70.2	366	4	US-10-425-115-267141	Sequence 267141, A
40	33	70.2	713	5	US-10-504-543-4	Sequence 4, Appl1
41	33	70.2	722	4	US-10-282-122A-53037	Sequence 53037, A
42	33	70.2	731	4	US-10-425-115-291856	Sequence 291856, A
43	33	70.2	991	4	US-10-425-115-303877	Sequence 303877, A
44	33	70.2	1057	4	US-10-425-115-290615	Sequence 290615, A
45	33	70.2	1062	4	US-10-425-115-271286	Sequence 271286, A

RESULT 1
US-10-353-929-14
; Sequence 14, Application US/10353929
; Publication No. US20030175288A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP01-1024
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: JP P2000-231814
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide having an ability to activate HLA-A2 restricted
; OTHER INFORMATION: Cytotoxic T Lymphocytes
US-10-353-929-14

Query Match 97.9%; Score 46; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1,7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
| | | | | | | | | |
DB 1 RIYDRKFL 9

RESULT 2
US-09-973-473-6
; Sequence 6, Application US/09973473
; Publication No. US20030041341A1
; GENERAL INFORMATION:
; APPLICANT: SONENBERG, Nahum
; APPLICANT: TREMBLAY, Michel
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
; TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
; FILE REFERENCE: 514012000400
; CURRENT APPLICATION NUMBER: US/09/973,473
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/CA00/00388
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,559
; PRIOR FILING DATE: 1999-04-09

;; PRIOR APPLICATION NUMBER: 60/179,743
;; PRIOR FILING DATE: 2000-02-02
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 6
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-973-473-6

Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 1 RIYDRKFL 9

RESULT 3

US-09-973-473-7
;; Sequence 7, Application US/09973473
;; Publication No. US20030041341A1
;; GENERAL INFORMATION:
;; APPLICANT: SONENBERG, Nahum
;; APPLICANT: TREMBLAY, Michel
;; APPLICANT: TSUKIYAMA-KOHARA, KYOKO
;; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
;; TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
;; FILE REFERENCE: 514012000400
;; CURRENT FILING DATE: 2001-10-03
;; PRIOR APPLICATION NUMBER: US/09/973,473
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: PCT/CA00/00388
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: 60/128,559
;; PRIOR FILING DATE: 1999-04-09
;; PRIOR APPLICATION NUMBER: 60/179,743
;; PRIOR FILING DATE: 2000-02-02
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 7
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-973-473-7

Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 1 RIYDRKFL 9

RESULT 4

US-09-973-473-8
;; Sequence 8, Application US/09973473
;; Publication No. US20030041341A1
;; GENERAL INFORMATION:
;; APPLICANT: SONENBERG, Nahum
;; APPLICANT: TREMBLAY, Michel
;; APPLICANT: TSUKIYAMA-KOHARA, KYOKO
;; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
;; TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
;; FILE REFERENCE: 514012000400
;; CURRENT FILING DATE: 2001-10-03
;; PRIOR APPLICATION NUMBER: US/09/973,473
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: PCT/CA00/00388
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: 60/128,559

;; PRIOR FILING DATE: 1999-04-09
;; PRIOR APPLICATION NUMBER: 60/179,743
;; PRIOR FILING DATE: 2000-02-02
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 8
;; LENGTH: 16
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-973-473-8

Query Match 97.9%; Score 46; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
Db 1 RIYDRKFL 9

RESULT 5

US-10-096-703-1
;; Sequence 1, Application US/10096703
;; Publication No. US20020132330A1
;; GENERAL INFORMATION:
;; APPLICANT: Hillman, Jennifer L.
;; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/096,703
;; FILING DATE: 12-Mar-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/215,063
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0310 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 100 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BSTMOT01
;; CLONE: 805296
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-096-703-1

Query Match 97.9%; Score 46; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9

Db 37 RIYDRKFL 45

RESULT 6

US-10-408-765A-416
Sequence 416, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Choeh, Sounlra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 416
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-416

Query Match 97.9%; Score 46; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 37 RIYDRKFL 45

RESULT 7

US-10-631-467-1617
Sequence 1617, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
TITLE OF INVENTION: disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: Patentin version 3.1
SEQ ID NO 1617
LENGTH: 117
TYPE: PRT
ORGANISM: Mus musculus
US-10-631-467-1617

Query Match 97.9%; Score 46; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 50 RIYDRKFL 58

RESULT 8
US-10-353-929-48
Sequence 48, Application US/10353929

Publication No. US20030175288A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-353-929-48

Query Match 97.9%; Score 46; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 9

US-10-631-467-917
Sequence 917, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
TITLE OF INVENTION: disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: Patentin version 3.1
SEQ ID NO 917
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-631-467-917

Query Match 97.9%; Score 46; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
Db 51 RIYDRKFL 59

RESULT 10

US-09-925-300-1267
Sequence 1267, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1267
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1267

Query Match 97.9%; Score 46; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
|||
Db 56 RIYDRKFL 64

RESULT 11
US-10-096-703-3
; Sequence 3, Application US/10096703
; Publication No. US20020132330A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,703
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/215,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 561632
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-096-703-3

Query Match 97.9%; Score 46; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
|||
Db 51 RIYDRKFL 59

RESULT 12
US-10-096-703-4
; Sequence 4, Application US/10096703
; Publication No. US20020132330A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,703
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/215,063
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0310 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1658516
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-096-703-4

Query Match 97.9%; Score 46; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIYDRKFL 9
|||
Db 51 RIYDRKFL 59

RESULT 13
US-09-925-301-1164
; Sequence 1164, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Roese et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1164
LENGTH: 138
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1164

Query Match
Best Local Similarity 97.9%; Score 46; DB 3; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
|||
Db 71 RIYDRKFL 79

RESULT 14

US-10-425-115-251396
Sequence 251396, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 251396
LENGTH: 63
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(63)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_160859C.1.pap
US-10-425-115-251396

Query Match
Best Local Similarity 89.4%; Score 42; DB 4; Length 63;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIYDRKFL 9
|||
Db 9 RIYDRKFL 17

RESULT 15
US-10-353-929-15
Sequence 15, Application US/10353929
Publication No. US20030175288A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Designed peptide having an ability to activate HLA-A2 restricted
OTHER INFORMATION: Cytotoxic T lymphocytes

US-10-353-929-15

Query Match
Best Local Similarity 87.2%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYDRKFL 9
|||
Db 1 IYDRKFL 8

Search completed: November 29, 2005, 23:10:28
Job time : 78.9545 secs

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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:45:19 (Search time 2.5 Seconds
(without alignments))
12.124 Million cell updates/sec

Title: US-10-019-198a-3
Perfect score: 47
Sequence: 1 RIIVDRKFLX 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdp.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdp.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdp.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdp.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdp.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdp.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdp.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	68.1	433	1	US-10-667-295-83 Sequence 83, Appl
2	32	68.1	434	1	US-10-667-295-141 Sequence 141, Appl
3	32	68.1	505	1	US-10-667-295-82 Sequence 82, Appl
4	32	68.1	506	1	US-10-667-295-140 Sequence 140, Appl
5	32	68.1	526	1	US-10-667-295-139 Sequence 139, Appl
6	32	68.1	534	1	US-10-667-295-81 Sequence 81, Appl
7	31	66.0	686	7	US-11-065-943-52 Sequence 52, Appl
8	28	59.6	396	7	US-11-022-562-228 Sequence 228, Appl
9	28	59.6	400	1	US-10-793-626-2774 Sequence 2774, Appl
10	28	59.6	429	1	US-10-793-626-3174 Sequence 3174, Appl
11	28	59.6	478	1	US-10-821-234-915 Sequence 915, Appl
12	27	57.4	251	7	US-11-054-515-1292 Sequence 1292, Appl
13	27	57.4	402	1	US-10-821-234-1581 Sequence 1581, Appl
14	27	57.4	477	1	US-10-131-826A-452 Sequence 452, Appl
15	27	57.4	1150	1	US-10-821-234-1083 Sequence 1083, Appl
16	26	55.3	70	1	US-10-994-820A-16 Sequence 16, Appl
17	26	55.3	120	1	US-10-994-820A-12 Sequence 12, Appl
18	26	55.3	120	1	US-10-994-820A-13 Sequence 13, Appl
19	26	55.3	152	1	US-10-994-820A-15 Sequence 15, Appl
20	26	55.3	157	1	US-10-994-820A-14 Sequence 14, Appl
21	26	55.3	194	1	US-10-994-820A-7 Sequence 7, Appl
22	26	55.3	224	1	US-10-994-820A-6 Sequence 6, Appl
23	26	55.3	231	1	US-10-994-820A-8 Sequence 8, Appl
24	26	55.3	259	1	US-10-994-820A-17 Sequence 17, Appl
25	26	55.3	266	1	US-10-793-626-212 Sequence 212, Appl

26	55.3	309	1	US-10-485-517-161 Sequence 161, Appl
27	55.3	309	1	US-10-994-820A-2 Sequence 2, Appl
28	55.3	310	1	US-10-994-820A-10 Sequence 10, Appl
29	55.3	321	1	US-10-793-626-2816 Sequence 2816, Appl
30	55.3	354	1	US-10-485-517-179 Sequence 179, Appl
31	55.3	354	1	US-10-485-517-179 Sequence 366, Appl
32	55.3	505	1	US-10-519-447-4 Sequence 4, Appl
33	55.3	591	1	US-10-485-517-332 Sequence 332, Appl
34	55.3	651	1	US-10-994-820A-34 Sequence 34, Appl
35	55.3	654	7	US-11-046-668-4 Sequence 4, Appl
36	55.3	683	7	US-11-046-668-2 Sequence 2, Appl
37	55.3	698	1	US-10-793-626-2388 Sequence 2388, Appl
38	55.3	709	7	US-11-074-176-158 Sequence 158, Appl
39	55.3	770	1	US-10-982-545-15 Sequence 38, Appl
40	55.3	770	1	US-10-789-273-38 Sequence 38, Appl
41	55.3	1094	1	US-10-821-234-1097 Sequence 1097, Appl
42	55.3	1170	1	US-10-858-730-71 Sequence 71, Appl
43	55.3	1189	1	US-10-821-234-1209 Sequence 1209, Appl
44	55.3	1338	1	US-10-821-234-1622 Sequence 1622, Appl
45	55.3	1338	7	US-11-109-156-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-667-295-83
Sequence 83, Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Masclia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 433
TYPE: PRP
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(433)
OTHER INFORMATION: Ceres Seq. ID no. 12558792
US-10-667-295-83

Query Match 68.1%, Score 32, DB 1, Length 433;
Best Local Similarity 62.5%, Pred. No. 7.2;
Matches 5, Conservative 3, Mismatches 0, Indels 0, Gaps 0;

QY 1 RIIVDRKF 8
DB 116 RIIVDRKF 123

RESULT 2
US-10-667-295-141
Sequence 141, Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Masclia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 141

```
LENGTH: 434
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(434)
; OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141
```

```
Query Match      68.1%; Score 32; DB 1; Length 434;
Best Local Similarity 62.5%; Pred. No. 7.2;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RIYDRKF 8
Db      116 RIMFDRRF 123
```

```
RESULT 3
US-10-667-295-82
; Sequence 82, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82
```

```
Query Match      68.1%; Score 32; DB 1; Length 505;
Best Local Similarity 62.5%; Pred. No. 8.3;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RIYDRKF 8
Db      188 RIMFDRRF 195
```

```
RESULT 4
US-10-667-295-140
; Sequence 140, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(506)
; OTHER INFORMATION: Ceres Seq. ID no. 13531807
```

```
US-10-667-295-140
```

```
Query Match      68.1%; Score 32; DB 1; Length 506;
Best Local Similarity 62.5%; Pred. No. 8.4;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RIYDRKF 8
Db      188 RIMFDRRF 195
```

```
RESULT 5
US-10-667-295-139
; Sequence 139, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(526)
; OTHER INFORMATION: Ceres Seq. ID no. 13531806
US-10-667-295-139
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```
Query Match      68.1%; Score 32; DB 1; Length 526;
Best Local Similarity 62.5%; Pred. No. 8.7;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RIYDRKF 8
Db      208 RIMFDRRF 215
```

```
RESULT 6
US-10-667-295-81
; Sequence 81, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(534)
; OTHER INFORMATION: Ceres Seq. ID no. 12558790
US-10-667-295-81
```

```
Query Match      68.1%; Score 32; DB 1; Length 534;
Best Local Similarity 62.5%; Pred. No. 8.8;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RIYDRKF 8
```

Db 217 RIMEDRRF 224

RESULT 7
US-11-065-943-52

Sequence 52, Application US/11065943
Publication No. US20050250131A1
GENERAL INFORMATION:
APPLICANT: JESTIN, JEAN-LUC
APPLICANT: VICHIER-GUERRE, SOPHIE
APPLICANT: FERRIS, STEPHANE
TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REFERENCE: 266426US0XCIP
CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn version 3.3
SEQ ID NO 52
LENGTH: 686
TYPE: PRT
ORGANISM: Bacillus circulans
US-11-065-943-52

Query Match 59.6%; Score 31; DB 7; Length 686;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYDRKF 8
419 IYERKF 425

Db 419 IYERKF 425

RESULT 8
US-11-022-562-228
Sequence 228, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DEN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 228
LENGTH: 396
TYPE: PRT
ORGANISM: Clostridium difficile
US-11-022-562-228

Query Match 59.6%; Score 28; DB 7; Length 396;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYDRKFL 9
213 IYQSKFL 220

Db 213 IYQSKFL 220

Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2774
LENGTH: 400
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2774

Query Match 59.6%; Score 28; DB 1; Length 400;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IYDRK 7
288 IYDRK 293

Db 288 IYDRK 293

RESULT 10
US-10-793-626-3174
Sequence 3174, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3174
LENGTH: 429
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3174

Query Match 59.6%; Score 28; DB 1; Length 429;
Best Local Similarity 37.5%; Pred. No. 44;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIYDRKF 8
348 QVYDVKY 355

Db 348 QVYDVKY 355

RESULT 11
US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Iyan
APPLICANT: Scache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

```
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 915
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-915
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Query Match          59.6%; Score 28; DB 1; Length 478;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      1 RIYDRKFL 9
Db      384 REAYDRDPL 392
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RESULT 12
US-11-054-515-1292
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; Sequence 1292, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
```

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; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
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; FILE REFERENCE: P5523P3
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; CURRENT APPLICATION NUMBER: US/11/054,515
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; CURRENT FILING DATE: 2005-02-10
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; PRIOR APPLICATION NUMBER: 60/543,296
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; PRIOR FILING DATE: 2004-02-11
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; PRIOR APPLICATION NUMBER: 60/580,347
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; PRIOR FILING DATE: 2004-06-18
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; PRIOR APPLICATION NUMBER: 10/293,418
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; PRIOR FILING DATE: 2002-11-14
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; PRIOR APPLICATION NUMBER: 60/331,469
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; PRIOR FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/340,817
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; PRIOR FILING DATE: 2001-12-19
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; PRIOR APPLICATION NUMBER: 09/880,748
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; PRIOR FILING DATE: 2001-06-15
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; PRIOR APPLICATION NUMBER: 60/293,499
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; PRIOR FILING DATE: 2001-05-25
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; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR FILING DATE: 2001-03-21
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; PRIOR APPLICATION NUMBER: 60/276,248
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; PRIOR FILING DATE: 2001-03-16
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; PRIOR APPLICATION NUMBER: 60/240,816
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; PRIOR FILING DATE: 2000-10-17
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; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 3247
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; SEQ ID NO 1292
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; LENGTH: 251
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-11-054-515-1292
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Query Match          57.4%; Score 27; DB 7; Length 251;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      4 YDRKFL 9
Db      60 YSRKFL 65
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RESULT 13
US-10-821-234-1581
; Sequence 1581, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Labat, Ivan
```

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; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
```

```
; CURRENT APPLICATION NUMBER: US/10/821,234
```

```
; CURRENT FILING DATE: 2004-04-07
```

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; PRIOR APPLICATION NUMBER: US 60/462,047
```

```
; PRIOR FILING DATE: 2003-04-07
```

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; NUMBER OF SEQ ID NOS: 1704
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; SOFTWARE: pt_seq_genes Version 1.0
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; SEQ ID NO 1581
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; LENGTH: 402
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-10-821-234-1581
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Query Match          57.4%; Score 27; DB 1; Length 402;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY      2 RIYDRKFL 9
Db      375 IIMDRPFL 382
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RESULT 14
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US-10-131-826A-452
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; Sequence 452, Application US/10131826A
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; Publication No. US20050245730A1
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; GENERAL INFORMATION:
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```
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Beresini, Maureen
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; APPLICANT: Deforge, Laura
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; APPLICANT: Desnoyers, Luc
```

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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
```

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; APPLICANT: Gerritsen, Mary E.
```

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; APPLICANT: Goddard, Audrey
```

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; APPLICANT: Godowski, Paul J.
```

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; APPLICANT: Gurney, Austin L.
```

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; APPLICANT: Sherwood, Steven
```

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; APPLICANT: Smith, Victoria
```

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; APPLICANT: Stewart, Timothy A.
```

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; APPLICANT: Tumas, Daniel
```

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; APPLICANT: Watanabe, Colin K
```

```
; APPLICANT: Wood, William
```

```
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; FILE REFERENCE: P3330R1C128
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; CURRENT APPLICATION NUMBER: US/10/131,826A
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; CURRENT FILING DATE: 2002-04-24
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; PRIOR APPLICATION NUMBER: 60/049911
```

```
; PRIOR FILING DATE: 1997-06-18
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; PRIOR APPLICATION NUMBER: 60/056974
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; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059122
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059184
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/059352
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; PRIOR FILING DATE: 1997-09-19
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; PRIOR APPLICATION NUMBER: 60/059588
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; PRIOR FILING DATE: 1997-09-19
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/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 550  
/ SEQ ID NO 452  
/ LENGTH: 477  
/ TYPE: PRT  
/ ORGANISM: Homo Sapien  
US-10-131-826A-452
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Query Match          57.4%; Score 27; DB 1; Length 477;  
Best Local Similarity 83.3%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      3 IYDRKF 8  
        |||||  
DB      111 IYDSKF 116
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RESULT 15  
US-10-821-234-1083  
/ Sequence 1083, Application US/10821234  
/ Publication No. US20050255114A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Labat, Ivan  
/ APPLICANT: Stache-Crain, Birgit  
/ APPLICANT: Andarmani, Susan  
/ APPLICANT: Tang, Y. Tom  
/ TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia  
/ FILE REFERENCE: 821A  
/ CURRENT APPLICATION NUMBER: US/10/821,234  
/ CURRENT FILING DATE: 2004-04-07  
/ PRIOR APPLICATION NUMBER: US 60/462,047  
/ PRIOR FILING DATE: 2003-04-07  
/ NUMBER OF SEQ ID NOS: 1704  
/ SOFTWARE: pt_seq_genes Version 1.0  
/ SEQ ID NO 1083  
/ LENGTH: 1150  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc_feature  
/ LOCATION: (1)..(1150)  
/ OTHER INFORMATION: Xaa = any amino acid or nothing  
US-10-821-234-1083
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Query Match          57.4%; Score 27; DB 1; Length 1150;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      1 RIYDRKFL 9  
        :|||  
DB      1008 QMIYQRPFL 1016
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Search completed: November 29, 2005, 23:04:38  
Job time : 2.75 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: November 29, 2005, 21:58:13 ; Search time 95.4546 Seconds
(without alignments)
46.030 Million cell updates/sec

Title: US-10-019-198a-5
Perfect score: 19
Sequence: 1 XXXYXXXXLX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneeqp1980a:*
- 2: geneeqp1990a:*
- 3: geneeqp2000a:*
- 4: geneeqp2001a:*
- 5: geneeqp2002a:*
- 6: geneeqp2003a:*
- 7: geneeqp2003ba:*
- 8: geneeqp2004a:*
- 9: geneeqp2005a:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	11	57.9	6 ABP83755	Abp83755 HLA prote
2	11	57.9	6 ABP84060	Abp84060 HLA prote
3	11	57.9	6 ABP84934	Abp84934 HLA prote
4	11	57.9	6 ABP84936	Abp84936 HLA prote
5	11	57.9	6 ABP85536	Abp85536 HLA prote
6	11	57.9	6 ABP85937	Abp85937 HLA prote
7	11	57.9	6 ABP86587	Abp86587 HLA prote
8	11	57.9	6 ABP87076	Abp87076 HLA prote
9	11	57.9	6 ABP87077	Abp87077 HLA prote
10	11	57.9	6 ABP88907	Abp88907 HLA prote
11	11	57.9	6 ABP89307	Abp89307 HLA prote
12	11	57.9	6 ABP84056	Abp84056 HLA prote
13	11	57.9	6 ABP84643	Abp84643 HLA prote
14	11	57.9	6 ABP85166	Abp85166 HLA prote
15	11	57.9	6 ABP86592	Abp86592 HLA prote
16	11	57.9	6 ABP87280	Abp87280 HLA prote
17	11	57.9	6 ABP88388	Abp88388 HLA prote
18	11	57.9	6 ABP88900	Abp88900 HLA prote
19	11	57.9	6 ABP88905	Abp88905 HLA prote
20	11	57.9	6 ABP89431	Abp89431 HLA prote
21	11	57.9	6 ABP83762	Abp83762 HLA prote
22	11	57.9	6 ABP84937	Abp84937 HLA prote
23	11	57.9	6 ABP85237	Abp85237 HLA prote
24	11	57.9	6 ABP87566	Abp87566 HLA prote

25	11	57.9	9 6 ABP87601	Abp87601 HLA prote
26	11	57.9	9 6 ABP88821	Abp88821 HLA prote
27	11	57.9	9 6 ABP88901	Abp88901 HLA prote
28	11	57.9	9 6 ABP89396	Abp89396 HLA prote
29	11	57.9	9 6 ABP90314	Abp90314 HLA prote
30	11	57.9	9 6 ABP90317	Abp90317 HLA prote
31	11	57.9	9 6 ABP84640	Abp84640 HLA prote
32	11	57.9	9 6 ABP84831	Abp84831 HLA prote
33	11	57.9	9 6 ABP85528	Abp85528 HLA prote
34	11	57.9	9 6 ABP86101	Abp86101 HLA prote
35	11	57.9	9 6 ABP88448	Abp88448 HLA prote
36	11	57.9	9 6 ABP88453	Abp88453 HLA prote
37	11	57.9	9 6 ABP88526	Abp88526 HLA prote
38	11	57.9	9 6 ABP88937	Abp88937 HLA prote
39	11	57.9	9 6 ABP89003	Abp89003 HLA prote
40	11	57.9	9 6 ABP89463	Abp89463 HLA prote
41	11	57.9	9 6 ABP90547	Abp90547 HLA prote
42	11	57.9	9 6 ABP84042	Abp84042 HLA prote
43	11	57.9	9 6 ABP84638	Abp84638 HLA prote
44	11	57.9	9 6 ABP85239	Abp85239 HLA prote
45	11	57.9	9 6 ABP85768	Abp85768 HLA prote

ALIGNMENTS

RESULT 1
ABP83755
ID ABP83755 standard; peptide; 9 AA.

XX ABP83755;

XX 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #110.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX humoral immune response; cellular immune response;

XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Challenge-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of

CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterizing domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;

Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
Db 1 YSTTTL 6

RESULT 2
ABP84060
ID ABP84060 standard; peptide; 9 AA.
XX
AC ABP84060;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #415.
XX

KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KM humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.

PN WO200283068-A2.

PD 24-OCT-2002.

PF 09-APR-2002; 2002WO-US011359.

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

PR 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

PI Challita-Eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

DR WPI; 2003-092956/08.

XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

PS Claim 13; Page 136; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterizing cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterizing domain-specific antibodies, for identifying

CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;

Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
Db 2 YSTTTL 7

RESULT 3
ABP84934
ID ABP84934 standard; peptide; 9 AA.
XX
AC ABP84934;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #1289.

KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KM humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.

PN WO200283068-A2.

PD 24-OCT-2002.

PF 09-APR-2002; 2002WO-US011359.

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

PR 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

PI Challita-Eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

DR WPI; 2003-092956/08.

XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

PS Claim 13; Page 153; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterizing cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterizing domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies

CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;

Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 4 YSTTTL 9

RESULT 4
ABP84936
ID ABP84936 standard; peptide; 9 AA.

XX ABP84936;
XX 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #1291.

XX Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX MO20283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

XX Claim 13; Page 153; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, 121P2A3. The composition of the
XX invention has cytostatic and immunostimulant activity, and is useful as a
XX vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes 121P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of 121P2A3 gene products
XX in normal versus cancerous tissues. The proteins are useful for
XX generating and characterising domain-specific antibodies, for identifying
XX agents or cellular factors that bind to 121P2A3 or a particular structure
XX domain, and in various therapeutic and diagnostic contexts, including
XX cancer vaccines. The antibodies or T cells reactive with the product are
XX useful in passive or active immunisation, and in imaging methodologies
XX for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX represent peptides from the 121P2A3 variants of the invention
SQ Sequence 9 AA;

Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 2 YSTTTL 7

RESULT 5
ABP85536
ID ABP85536 standard; peptide; 9 AA.

XX ABP85536;

XX 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #1891.

XX Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX MO20283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

XX Claim 13; Page 165; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, 121P2A3. The composition of the
XX invention has cytostatic and immunostimulant activity, and is useful as a
XX vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes 121P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of 121P2A3 gene products
XX in normal versus cancerous tissues. The proteins are useful for
XX generating and characterising domain-specific antibodies, for identifying
XX agents or cellular factors that bind to 121P2A3 or a particular structure
XX domain, and in various therapeutic and diagnostic contexts, including
XX cancer vaccines. The antibodies or T cells reactive with the product are
XX useful in passive or active immunisation, and in imaging methodologies
XX for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX represent peptides from the 121P2A3 variants of the invention
SQ Sequence 9 AA;

Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Oy      4 YXXXXL 9
      |         |
Db      2 YSTTTL 7

RESULT 6
ABP85937
ID ABP85937 standard; peptide; 9 AA.
XX
AC ABP85937;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #2292.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KM humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011359.
XX
PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
PR 22-JUN-2001; 2001US-0300373P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raicano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
DR WPI; 2003-092956/08.
XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.
XX
PS Claim 13; Page 175; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;

Query Match      57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 7
ABP8587
ID ABP8587 standard; peptide; 9 AA.
XX
AC ABP8587;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #2942.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KM humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011359.
XX
PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
PR 22-JUN-2001; 2001US-0300373P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raicano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
DR WPI; 2003-092956/08.
XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.
XX
PS Claim 13; Page 182; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;

Query Match      57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```


KM Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011359.
XX
PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
PR 22-JUN-2001; 2001US-0300373P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-092956/08.
XX
DR
XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.
XX
PS Claim 13; Page 204; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;
XX
Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 4 YXXXXL 9
Db 2 YSTTTL 7
XX
RESULT 11
ABP89307
ID ABP89307 standard; peptide; 9 AA.
XX
AC ABP89307;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #5662.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX

OS Homo sapiens.
XX
PN WO200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011359.
XX
PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
PR 22-JUN-2001; 2001US-0300373P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-092956/08.
XX
DR
XX
PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.
XX
PS Claim 13; Page 208; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 9 AA;
XX
Query Match 57.9%; Score 11; DB 6; Length 9;
Best Local Similarity 33.3%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 4 YXXXXL 9
Db 1 YSTTTL 6
XX
RESULT 12
ABP84056
ID ABP84056 standard; peptide; 9 AA.
XX
AC ABP84056;
XX
DT 28-MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #411.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283068-A2.
XX

PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US011359.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-Rid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 DR WPI; 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 136; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterizing cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterizing domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 SQ Sequence 9 AA;
 QY
 DB 4 YXXXXL 9
 3 YSTTTL 8
 Query Match 57.9%; Score 11; DB 6; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2e+06;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 RESULT 13
 ABP84643
 ID ABP84643 standard; peptide; 9 AA.
 XX
 AC ABP84643;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #998.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US011359.
 XX

PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-Rid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 DR WPI; 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 147; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterizing cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterizing domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 SQ Sequence 9 AA;
 QY
 DB 4 YXXXXL 9
 3 YSTTTL 8
 Query Match 57.9%; Score 11; DB 6; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2e+06;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 RESULT 14
 ABP85166
 ID ABP85166 standard; peptide; 9 AA.
 XX
 AC ABP85166;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #1521.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US011359.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX

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OM protein - protein search, using BW model

Run on: November 29, 2005, 22:35:24 ; Search time 15.6818 Seconds
(without alignments)
61.356 Million cell updates/sec

Title: US-10-019-198a-5
Perfect score: 19
Sequence: 1 XXXXXXXXXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	57.9	15	2	PH1314	Ig heavy chain DJ
2	11	57.9	38	2	D82306	hypothetical prote
3	11	57.9	46	2	E85743	hypothetical prote
4	11	57.9	54	2	UT0521	Ig kappa chain V-1
5	11	57.9	61	2	E39741	14k hypothetical t
6	11	57.9	68	1	JN0537	head protein gp3 -
7	11	57.9	68	2	P90970	probable head comp
8	11	57.9	69	1	QOV27	hypothetical prote
9	11	57.9	69	2	F42516	D-OR-C protein -
10	11	57.9	71	2	S21526	Ig kappa chain V r
11	11	57.9	76	2	T17673	hypothetical prote
12	11	57.9	81	2	C89872	hypothetical prote
13	11	57.9	81	2	C89706	conserved hypotet
14	11	57.9	86	2	S34086	Ig kappa chain V r
15	11	57.9	86	2	S16840	Ig kappa chain V r
16	11	57.9	87	2	S34084	Ig kappa chain V r
17	11	57.9	87	2	S21523	Ig kappa chain V r
18	11	57.9	87	2	S34083	Ig kappa chain V r
19	11	57.9	88	2	S21525	Ig kappa chain V r
20	11	57.9	88	2	S21522	Ig kappa chain V r
21	11	57.9	88	2	S21528	Ig kappa chain V r
22	11	57.9	88	2	S21520	Ig kappa chain V r
23	11	57.9	88	2	S34104	Ig kappa chain V r
24	11	57.9	88	2	S21524	Ig kappa chain V r
25	11	57.9	88	2	PL0261	Ig kappa chain V r
26	11	57.9	90	2	B56273	sekacin A immunity
27	11	57.9	91	2	S17622	Ig kappa chain V r
28	11	57.9	91	2	UQ2204	hypothetical 10.7k
29	11	57.9	93	2	D71874	hypothetical prote

30	11	57.9	94	2	A01955	Ig kappa-B5 chain
31	11	57.9	95	2	S45324	Ig kappa chain V r
32	11	57.9	95	2	S65989	Ig kappa chain V r
33	11	57.9	95	2	PH0863	Ig kappa chain V r
34	11	57.9	98	2	PH1062	Ig light chain V r
35	11	57.9	101	2	S44117	Ig kappa chain V-J
36	11	57.9	101	2	C28840	Ig kappa chain V r
37	11	57.9	101	2	B28840	Ig kappa chain V r
38	11	57.9	101	2	B37262	Ig kappa chain V r
39	11	57.9	104	2	F87731	protein W10C8.2 (i
40	11	57.9	105	2	S36266	Ig lambda chain V
41	11	57.9	106	2	PL0260	Ig kappa chain V r
42	11	57.9	106	2	PL0259	Ig kappa chain V r
43	11	57.9	106	2	PL0262	Ig kappa chain V r
44	11	57.9	107	2	S36264	Ig lambda chain V
45	11	57.9	107	2	S36262	Ig lambda chain V

ALIGNMENTS

RESULT 1
PH1314
Ig heavy chain DJ region (clone C200-98) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #ext_change 07-May-1999
C/Accession: PH1314
R/Maserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1314
A/Molecule type: DNA
A/Residues: 1-15 <MAS>
A/Cross-references: UNIPARC:UPI000017C235
C/Keywords: heterotetramer; immunoglobulin

Query Match 57.9%; Score 11; DB 2; Length 15;
Best local Similarity 33.3%; Pred. No. 89;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 2 YSSSSL 7

RESULT 2
D82306
hypothetical protein VC0584 (imported) - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #ext_change 09-Jul-2004
C/Accession: D82306
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bas, S.; Qin, H.; Dragoi, I.; Sellers,
I.; R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of Both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82306
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-38 <HEI>
A/Cross-references: UNIPROT:Q9KUD8; UNIPARC:UPI00000C2D29; GB:AE004143; GB:AE003852; N1
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genes:
A/Gene: VC0584
A/Map position: 1

Query Match 57.9%; Score 11; DB 2; Length 38;
Best local Similarity 33.3%; Pred. No. 1,8e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9

Db 30 YSTSL 35

RESULT 3

E85743

hypothetical protein 22363 [imported] - Escherichia coli (strain O157:H7, substrain EDL8

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: E85743; B85717

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Hiller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: B85743

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-46 <STO>

A/Cross-references: UNIPROT:O8XC12; UNIPARC:UPI00001657A2; GB:AEO05174; NID:g12515355; F

A/Experimental source: strain O157:H7, substrain EDL933

A/Accession: B85717

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-46 <ST2>

A/Cross-references: UNIPARC:UPI00001657A2; GB:AEO05174; NID:g12515086; PIDN:AA656198.1;

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z2363; Z2132

Query Match 57.9%; Score 11; DB 2; Length 46;

Best Local Similarity 33.3%; Pred. No. 2e+02;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 13 YTAASL 18

RESULT 4

JT0521

IG kappa chain V-III region (Cp1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997

C/Accession: JT0521

R/Anker, R.; Conley, M.E.; Pollock, B.A.

J. Exp. Med. 169, 2109-2119, 1989

A/Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobu

A/Reference number: JT0511; MUID:89279157; PMID:2786547

A/Accession: JT0521

A/Molecule type: mRNA

A/Residues: 1-54 <ANK>

A/Cross-references: UNIPARC:UPI0000176D89

A/Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-49/Domain: V region <VRB>

F:50-54/Domain: J region <JRB>

Query Match 57.9%; Score 11; DB 2; Length 54;

Best Local Similarity 33.3%; Pred. No. 2.3e+02;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 4 YXXXXL 9

1 YAASSL 6

RESULT 5

E39741

14k hypothetical thioredoxin-related cyx3' region protein - Bradyrhizobium japonicum

C/Species: Bradyrhizobium japonicum

C/Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004

C/Accession: E39741

R/Ramseier, T.M.; Winteler, H.V.; Hennecke, H.

J. Biol. Chem. 266, 7793-7803, 1991

A/Title: Discovery and sequence analysis of bacterial genes involved in the biogenesis o

A/Reference number: A39741; MUID:91210304; PMID:1850420

A/Accession: E39741

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-61 <RAM>

A/Cross-references: UNIPROT:P30959; UNIPARC:UPI000005E784; GB:M60874; NID:g152073; PIDN:f

C/Keywords: transmembrane protein

Query Match 57.9%; Score 11; DB 2; Length 61;

Best Local Similarity 33.3%; Pred. No. 2.5e+02;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 4 YXXXXL 9

16 YAAAML 21

RESULT 6

JN0537

head protein gp3 - phage 21

C/Species: phage 21

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C/Accession: JN0537; C49849

R/Smith, M.P.; Feisls, M.

Gene 126, 1-7, 1993

A/Title: Sequence analysis of the phage 21 genes for prohead assembly and head completio

A/Reference number: JN0537; MUID:93231520; PMID:8472949

A/Accession: JN0537

A/Molecule type: DNA

A/Residues: 1-68 <SM1>

A/Cross-references: UNIPROT:P36271; UNIPARC:UPI0000138495; GB:M81255; NID:g215454; PIDN:f

R/Smith, M.P.; Feisls, M.

J. Bacteriol. 175, 2393-2399, 1993

A/Title: Sites and gene products involved in lambdaoid phage DNA packaging.

A/Reference number: A49849; MUID:93224462; PMID:8468297

A/Accession: C49849

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-27 <SM2>

A/Cross-references: UNIPARC:UPI0000174BC3

A/Note: sequence extracted from NCBI backbone (NCBI:129221, NCBI:129224)

C/Genetics:

C/Superfamily: phage lambda head-to-tail joining protein W

Query Match 57.9%; Score 11; DB 1; Length 68;

Best Local Similarity 33.3%; Pred. No. 2.7e+02;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 4 YXXXXL 9

35 YTAASL 40

RESULT 7

F90970

probable head completion protein [imported] - Escherichia coli (strain O157:H7, substrain

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004

C/Accession: F90970

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A/Reference number: A9629; MUID:21156231; PMID:11258796

A/Accession: F90970

A/Status: preliminary

A/Molecule type: DNA

A:Residues: 1-68 <HAY>
A:Cross-references: UNIPROT:Q8XC12; UNIPARC:UPI00000D0524; GB:BA000007; PIDN:BA036157.1;
A:Experimental source: strain 0157:H7, substrain RIMD 0509952
A:Genetics: EC82734
A:Gene: EC82734

Query Match 57.9%; Score 11; DB 2; Length 68;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 35 YTAASL 40

RESULT 8

Q0VZ7
hypothetical protein D-69 - vaccinia virus (strain WR)

C:Species: vaccinia virus

C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C:Accession: A03878

R:Nilges, E.G.; Condit, R.C.; Caro, P.; Davidson, K.; Matusick, L.; Seto, J.

Virology 153, 96-112, 1986

A:Title: Nucleotide sequence and genetic map of the 16-kb vaccinia virus HindIII D fragm

A:Reference number: A01146; MUID:86291159; PMID:3739227

A:Accession: A03878

A:Molecule type: DNA

A:Residues: 1-69 <NLT>

A:Cross-references: UNIPROT:P04304; UNIPARC:UPI00000013BC; GB:M15058

C:Superfamily: vaccinia virus D-ORF-C protein

Query Match 57.9%; Score 11; DB 1; Length 69;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 8 YASSSL 13

RESULT 9

F42516
D-ORF-C protein - vaccinia virus (strain Copenhagen)

C:Species: vaccinia virus

A:Note: host Homo sapiens (man)

C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004

C:Accession: F42516

R:Johnson, G.P.

submitted to GenBank, June 1990

A:Reference number: A33172

A:Accession: F42516

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-69 <JOH>

A:Cross-references: UNIPROT:P20552; UNIPARC:UPI000013C1D1

C:Superfamily: vaccinia virus D-ORF-C protein

Query Match 57.9%; Score 11; DB 2; Length 69;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 8 YASSSL 13

RESULT 10

S21526

IG kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999

C:Accession: S34082; S21526

R:Magner, S.D.; Iuzatco, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <W42>

A:Cross-references: UNIPARC:UPI000011604F; EMBL:X66042; NID:g33318; PIDN:CAA46841.1; PIB

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 57.9%; Score 11; DB 2; Length 71;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 42 YAASTL 47

RESULT 11

T17673
hypothetical protein a183L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T17673

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T17673

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-76 <GRA>

A:Cross-references: UNIPROT:Q84503; UNIPARC:UPI0000F0E0D; EMBL:U42580; NID:g4028896; PIB

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics: a183L

Query Match 57.9%; Score 11; DB 2; Length 76;
Best Local Similarity 33.3%; Pred. No. 3e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 37 YAAASL 42

RESULT 12

C89872
hypothetical protein [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: C89872

R:Kuroda, M.; Ohra, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizumatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89872

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-81 <KUR>

A:Cross-references: UNIPROT:Q99V57; UNIPARC:UPI00000D76BD; GB:BA000018; PID:g13700838; PIB

A:Experimental source: strain N315

C:Genetics: SA0889

A:Gene: SA0889

Query Match 57.9%; Score 11; DB 2; Length 81;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9

Db 27 YTAASL 32

RESULT 13
F87306 conserved hypothetical protein CC0463 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87306
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-84 <STO>
A:Cross-references: UNIPROT:Q9AAX9; UNIPARC:UPI000013984D; GB:AE005673; MID:G13421636; F
A:Gene: CC0463
C:Superfamily: conserved hypothetical protein H11000

Query Match 57.9%; Score 11; DB 2; Length 84;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
| |
Db 36 YTAAML 41

RESULT 14
S34086 Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34086
R:Wagner, S.D.; Luzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>
A:Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176D9E; EMBL:X67169
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 11; DB 2; Length 86;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
| |
Db 42 YTAASL 47

RESULT 15
S16840 Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S16840
R:Blaisson, G.; Kuntz, J.L.; Paquati, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16840

A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176DA5; EMBL:X54838
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 11; DB 2; Length 86;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
| |
Db 40 YTAASL 45

Search completed: November 29, 2005, 23:02:35
Job time : 17.6818 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 29, 2005, 22:35:04 ; Search time 95.9091 Seconds
(without alignments)
73.562 Million cell updates/sec

Title: US-10-019-198a-5
Perfect score: 19
Sequence: 1 XXXXXXXXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_05.80.*
1: UniProt_sprot.*
2: UniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	57.9	23	2	Q5BXT1 SCHJA
2	11	57.9	35	2	Q5UM11_FRAAN
3	11	57.9	37	2	Q4YIV5_PLABE
4	11	57.9	38	2	Q9KUD8_VIBCH
5	11	57.9	46	2	Q8XC12_ECOS7
6	11	57.9	49	2	Q6CVL2_KLUJA
7	11	57.9	49	2	Q9AFM3_SHIFL
8	11	57.9	51	2	Q57GG2_SALCL
9	11	57.9	53	2	Q6KSL8_BACOL
10	11	57.9	61	1	CCMD_BRAJA
11	11	57.9	61	2	Q6BKJ7_DEBHA
12	11	57.9	61	2	Q8VMA9_RHLET
13	11	57.9	62	2	Q5YFQ4_VYIRU
14	11	57.9	62	2	Q5GAB8_VYIRU
15	11	57.9	63	2	Q6GZU3_FRGIV
16	11	57.9	63	2	Q6YH61_VYIRU
17	11	57.9	64	2	Q6ZKG6_ORYSA
18	11	57.9	67	2	Q7UD80_SHIFL
19	11	57.9	68	1	VG03_BP21
20	11	57.9	68	1	VG03_EC06
21	11	57.9	68	2	Q7ACV9_ECOS7
22	11	57.9	68	2	Q5PAUG_ANAMM
23	11	57.9	68	2	Q8F1H6_EC06
24	11	57.9	69	1	YVDC_VACCC
25	11	57.9	69	1	YVDC_VACCC
26	11	57.9	69	2	Q9AM51_BRAJA
27	11	57.9	69	2	Q7MRV7_WOLIS
28	11	57.9	69	2	Q775T4_CAMPS
29	11	57.9	71	2	Q67W10_ORYSA
30	11	57.9	72	2	Q6CB16_YARLI
31	11	57.9	73	2	Q691A7_PIPJA

32	11	57.9	76	2	Q7XIJ7_ORYSA	Q7XIJ7_oryza sativ
33	11	57.9	76	2	Q84503_CHYPI	Q84503_parmecium
34	11	57.9	76	2	Q4JNG9_9HEPC	Q4JNG9_hepatitis c
35	11	57.9	76	2	Q4JNH0_9HEPC	Q4JNH0_hepatitis c
36	11	57.9	76	2	Q4JNH1_9HEPC	Q4JNH1_hepatitis c
37	11	57.9	76	2	Q4JNH2_9HEPC	Q4JNH2_hepatitis c
38	11	57.9	76	2	Q4JNH3_9HEPC	Q4JNH3_hepatitis c
39	11	57.9	76	2	Q4JNH4_9HEPC	Q4JNH4_hepatitis c
40	11	57.9	76	2	Q4JNH5_9HEPC	Q4JNH5_hepatitis c
41	11	57.9	76	2	Q4JNH6_9HEPC	Q4JNH6_hepatitis c
42	11	57.9	76	2	Q4JNH7_9HEPC	Q4JNH7_hepatitis c
43	11	57.9	76	2	Q4JNH8_9HEPC	Q4JNH8_hepatitis c
44	11	57.9	76	2	Q4JNH9_9HEPC	Q4JNH9_hepatitis c
45	11	57.9	79	2	Q5BTH0_SCHJA	Q5BTH0_schistosoma

ALIGNMENTS

RESULT 1
Q5BXT1 SCHJA PRELIMINARY; PRT; 23 AA.
ID Q5BXT1 SCHJA PRELIMINARY; PRT; 23 AA.
AC Q5BXT1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypochemical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6182;
OK NCBI_Taxid=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY111905; AX27794.1; -, mRNA.
KW Hypochemical protein.
SQ SEQUENCE 23 AA; 2622 MW; 473EC523C9AF9967 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
Db 2 YSSSSL 7

RESULT 2

Q5UM11_FRAAN PRELIMINARY; PRT; 35 AA.
ID Q5UM11_FRAAN PRELIMINARY; PRT; 35 AA.
AC Q5UM11;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Glycosyltransferase family protein 47 (Frigment).
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_Taxid=3747;
OK NCBI_Taxid=3747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Balogh A., Koncz T., Kiss E., Heeszy L.E.;
RT "Identification of novel genes involved in ripening of strawberry
fruits";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY679583; AA33443.1; -, mRNA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 1 1
FT NON_TER 35 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3645 MW; FFA703CBA45C8A39 CRC64;

```

Query Match          57.9%; Score 11; DB 2; Length 35;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YXXXXL 9
Db 15 YVASSL 20

RESULT 3
Q4YLVS_PLABE PRELIMINARY; PRT; 37 AA.
ID Q4YLVS
AC Q4YLVS;
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB400696.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OK NCBI_TaxId=5821;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA James C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA101003773; CA101006.1; -; Genomic_DNA.
FT Hypothetical protein.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4157 MW; A985180238305DB9 CRC64;

Query Match          57.9%; Score 11; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YXXXXL 9
Db 19 YVSSSL 24

RESULT 4
Q9KUD8_VIBCH PRELIMINARY; PRT; 38 AA.
ID Q9KUD8;
AC Q9KUD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VC0584.
GN OrderedLocustNames=VC0584;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OK NCBI_TaxId=666;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gilm M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bess S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Uitterback T.R., Fleischmann R.D.,

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RA Niernan W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Melakias J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004143; AAF93751.1; -; Genomic_DNA.
DR PIR; D82306; D82306.
DR TIGR; VC0584; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 38 AA; 4133 MW; BA86FA65822A8899 CRC64;

Query Match          57.9%; Score 11; DB 2; Length 38;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YXXXXL 9
Db 30 YSTSL 35

RESULT 5
Q8XC12_EC057 PRELIMINARY; PRT; 46 AA.
ID Q8XC12_EC057
AC Q8XC12;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative head completion protein of prophage CP-9330 (Putative DNA
DE packaging protein of prophage CP-933R).
GN OrderedLocustNames=22132.22363;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxId=83334;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller U.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005174; AAG56196.1; -; Genomic_DNA.
DR EMBL; AE005174; AAG56409.1; -; Genomic_DNA.
DR PIR; E85743; E85743.
DR PIR; F90970; F90970.
DR HSSP; P03727; 1HYW.
DR GO; GO:0019067; P:Viral assembly, maturation, egress, and rel. .; IEA.
DR InterPro; IPR004174; gpm.
DR Pfam; PF02831; gpm; 1.
KW Complete proteome.
SQ SEQUENCE 46 AA; 5241 MW; 4FE2B985429B617C CRC64;

Query Match          57.9%; Score 11; DB 2; Length 46;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 YXXXXL 9
Db 13 YTAASL 18

RESULT 6
Q6CVL2_KULIA PRELIMINARY; PRT; 49 AA.
ID Q6CVL2_KULIA
AC Q6CVL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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DE KluYveromyces lactis strain NRRL Y-1140 chromosome B of strain NRRL Y-
DE 1140 of KluYveromyces lactis.
GN OrderedLocuNames=KLU0B1187g;
OS KluYveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; KluYveromyces.
OX NCBI_TaxID=28985;
RX PubMed=15229592; DOI=10.1038/nature02579;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeilise C., Talla B.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cartolico L., Confanioli F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,
RA Hantaye F., Hennequin C., Jouniaux N., Joyet P., Kichori R.,
RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Ozaa S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekla F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarcelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL: CR382122; CAH02420.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 49 AA; 5757 MW; DFC6B57DB186E80 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 29 YAAAML 34

RESULT 7
O9AFM3_SHIFL O9AFM3 SHIFL PRELIMINARY; PRT; 49 AA.
ID O9AFM3;
AC O9AFM3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orl, hypothetical.
OS Name=yacB;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RX PubMed=21189246; PubMed=11292750;
RX DOI=10.1128/IAI.69.5.3271-3285.2001;
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
RA Blattner F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
RT Shigella flexneri.";
RL Infect. Immun. 69:3271-3285 (2001).
DR EMBL: AF348706; AAK18546.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 49 AA; 5174 MW; 81FBCDF34312CA0 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 12 YSASL 17

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RESULT 8
O57GG2_SALCH O57GG2 SALCH PRELIMINARY; PRT; 51 AA.
ID O57GG2;
AC O57GG2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=SC4294;
OS Salmonella cholerae-suis (Salmonella enterica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RX PubMed=15781495;
RX SRRAIN=SC-867;
RA Chu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698 (2005).
DR EMBL: AB017220; AAK68200.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 5645 MW; BF41842EBDF831DB CRC64;

Query Match 57.9%; Score 11; DB 2; Length 51;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 26 YTTTSL 31

RESULT 9
O6XSL8_BACOL O6XSL8 BACOL PRELIMINARY; PRT; 53 AA.
ID O6XSL8;
AC O6XSL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE ATP synthase F0 subunit 8.
OS Bactrocera oleae (Olive fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Bactrocera; Dacnusa.
OX NCBI_TaxID=104688;
RX PubMed=14986921; DOI=10.1046/j.1365-2583.2003.00445.x;
RA Nardi F., Carapelli A., Dallai R., Frati F.;
RT "The mitochondrial genome of the olive fly Bactrocera oleae: two
RT haplotypes from distant geographical locations.";
RL Insect Mol. Biol. 12:605-611 (2003).
DR EMBL: AY210703; AA034658.1; -; Genomic_DNA.
DR EMBL: AY210702; AA034645.1; -; Genomic_DNA.
DR GO: GO:0016020; C:mitochondrion; IEA.
DR GO: GO:0005739; C:membrane; IEA.
DR GO: GO:0045263; C:proton-transporting ATP synthase complex; IEA.
DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
DR GO: GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR GO: GO:0015992; P:proton transport; IEA.
DR InterPro: IPR001421; ATPase8_mit.
DR Pfam: PF00895; ATP-8ynt 8; 1.
KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
KW Transmembrane; Transport.

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SEQ SEQUENCE 53 AA; 6256 MW; 110D4BE52DCB13C5 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 53;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 44 YSTTSL 49

RESULT 10

CCMD BRAJA STANDARD; PRT; 61 AA.
ID C30359;
AC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Heme exporter protein D (Cytochrome c-type biogenesis protein cycX).
GN Name=cycX; Synonyms=cmd; OrderedLocustNames=bsr0470;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
ON NCBI_TaxID=375;
OX [1]
NP NUCLEOTIDE SEQUENCE.
RP STRAIN=USDA 110R1F15;
RX MEDLINE=91210304; PubMed=1850420;
RA Rameier T.M., Winteler H.V., Hennecke H.;
RT "Discovery and sequence analysis of bacterial genes involved in the
biogenesis of c-type cytochromes."
RL J. Biol. Chem. 266:7793-7803(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneo T., Nakamura Y., Sato S., Minamitsawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriuchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
CC -1- FUNCTION: Required for the export of heme to the periplasm for the
biogenesis of c-type cytochromes (Potential).
CC -1- SIMILARITY: Belongs to the cmd/cycX/held family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; M60874; AAA26195.1; -; Genomic DNA.
DR EMBL; BA000040; BAC45735.1; -; Genomic DNA.
DR PIR; E39741; E39741.
DR InterPro; IPR007078; Cmd.
DR Pfam; PF04995; Cmd; 1.
KW Complete proteome; Cytochrome c-type biogenesis; Inner membrane;
KW Membrane; Transmembrane; Transport.
FT TRANSMEM 11 31 Potential.
SQ SEQUENCE 61 AA; 6776 MW; BCB9852E927370A CRC64;

Query Match 57.9%; Score 11; DB 1; Length 61;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 16 YAAAL 21

RESULT 11

O6BXJ7 DEBHA PRELIMINARY; PRT; 61 AA.

AC O6BXJ7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similarity.
GN OrderedLocustNames=DEHA0B02453g;
OS Debaryomyces hanseni (Yeast) (Torulasporea hanseni).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
ON NCBI_TaxID=4959;
OX [1]

NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durren P., Casaregola S., Talla E.,
RA Lafontaine I., de Montigny J., Marcq C., Neveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barry S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boirame A., Boyer J., Catolico L., Confantolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382134; CAG95060.1; -; Genomic DNA.
KW Complete proteome.

SEQ SEQUENCE 61 AA; 6684 MW; C2F6F79253E6A18 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 61;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 2 YSSSL 7

RESULT 12

O8VMA9 RHET PRELIMINARY; PRT; 61 AA.
AC O8VMA9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DAP decarboxylase (Fragment).
GN Name=LYSA;
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
ON NCBI_TaxID=29449;
OX [1]

NP NUCLEOTIDE SEQUENCE.
RP STRAIN=CE3;
RX MEDLINE=22031767; PubMed=12036281;
RA Ferraioli S., Tate R., Cernola M., Favre R., Iaccarino M.,
RA Patriarca E.J.;
RT "Auxotrophic mutant strains of Rhizobium etli reveal new nodule
development phenotypes."
RL Mol. Plant Microbe Interact. 15:501-510(2002).
DR EMBL; AJ422134; CAD19513.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 61 61
SQ SEQUENCE 61 AA; 6955 MW; B94868D845DA89A CRC64;

Query Match 57.9%; Score 11; DB 2; Length 61;

Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 31 YSTATL 36

RESULT 13

OSYFO4_GVIRU PRELIMINARY; PRT; 62 AA.

AC OSYFO4; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Hypothetical protein.

GN ORFNames=ORF011L;

OS Singapore grouper Iridovirus.

OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.

OX NCBI_TaxID=262968;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Song W.J., Qin Q.W., Qiu J., Huang C.H., Wang F., Hew C.L.;

RT "Functional Genomics Analysis of Singapore Grouper Iridovirus:

Complete Sequence Determination and Proteomic Analysis.";

RL J. Virol. 78:12576-12590(2004).

DR EMBL: AY521625; AAS18026.1; -; Genomic_DNA.

KM Hypothetical protein.

SO SEQUENCE 62 AA; 6634 MW; C7B664F54B70AC86 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 62;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 13 YSSAAL 18

RESULT 14

OSGAB8_GVIRU PRELIMINARY; PRT; 62 AA.

AC OSGAB8; 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DE Hypothetical protein.

GN ORFNames=GIV98;

OS Grouper Iridovirus.

OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.

OX NCBI_TaxID=127569;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA PubMed=15681403; DOI=10.1128/JVI.79.4.2010-2023.2005;

RT "Complete genome sequence of the grouper Iridovirus and comparison of

genomic organization with those of other Iridoviruses.";

RL J. Virol. 79:2010-2023(2005).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Chang C.-Y., Teal C.-T.;

RT "The complete genome sequence of Grouper Iridovirus,";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Murail S., Wu M.-F., Chang C.-Y.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE.

RA Chang C.-Y., Teal C.-T.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY666015; AAV91125.1; -; Genomic_DNA.

KM Hypothetical protein.

SO SEQUENCE 62 AA; 6634 MW; C7B664F54B70AC86 CRC64;

Query Match 57.9%; Score 11; DB 2; Length 62;

Best Local Similarity 33.3%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 13 YSSAAL 18

RESULT 15

OSGZU3_FRG3V PRELIMINARY; PRT; 63 AA.

AC OSGZU3; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

GN Frog virus 3 (FV3).

OS Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.

OX NCBI_TaxID=10493;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=Rana pipiens;

RX PubMed=15155820; DOI=10.1016/j.virol.2004.02.019;

RT Tan W.G., Barkman T.J., Gregory Chinchar V., Essani K.;

"Comparative genomic analyses of frog virus 3, type species of the

RT genus Ranavirus (family Iridoviridae).";

RL Virology 323:70-84(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=Rana pipiens;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY548484; AAT09692.1; -; Genomic_DNA.

KM Hypothetical protein.

SO SEQUENCE 63 AA; 6613 MW; 8ACC91B6139C0C8E CRC64;

Query Match 57.9%; Score 11; DB 2; Length 63;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 14 YSSAAL 19

Search completed: November 29, 2005, 23:01:24
Job time : 97.9091 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 29, 2005, 22:45:04 ; Search time 23.8636 Seconds
(without alignments)
34.645 Million cell updates/sec

Title: US-10-019-198A-5
Perfect score: 19
Sequence: 1 XXXXXXXXX 10

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCNUS.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	57.9	11	US-08-540-412-123	Sequence 123, App
2	11	57.9	11	US-08-540-412-191	Sequence 191, App
3	11	57.9	11	US-09-051-342-123	Sequence 123, App
4	11	57.9	11	US-09-051-342-191	Sequence 191, App
5	11	57.9	11	US-08-468-161-123	Sequence 123, App
6	11	57.9	11	US-09-051-759-123	Sequence 123, App
7	11	57.9	11	US-09-051-759-191	Sequence 191, App
8	11	57.9	11	US-09-051-759-123	Sequence 123, App
9	11	57.9	18	PCT-US95-08156-123	Sequence 123, App
10	11	57.9	20	US-09-513-365A-5	Sequence 5, App1
11	11	57.9	37	US-08-905-223-22	Sequence 22, App1
12	11	57.9	37	US-09-247-155-22	Sequence 22, App1
13	11	57.9	37	US-09-663-600A-22	Sequence 22, App1
14	11	57.9	37	US-09-903-190-22	Sequence 22, App1
15	11	57.9	40	US-08-812-586-40	Sequence 40, App1
16	11	57.9	40	US-09-535-832A-37	Sequence 37, App1
17	11	57.9	47	US-09-902-540-10080	Sequence 10080, A
18	11	57.9	54	US-09-640-211A-933	Sequence 933, App
19	11	57.9	60	US-09-248-796A-23819	Sequence 23819, A
20	11	57.9	61	US-09-248-796A-26016	Sequence 26016, A
21	11	57.9	62	US-09-248-796A-22643	Sequence 22643, A
22	11	57.9	64	US-09-107-532A-4990	Sequence 4990, App
23	11	57.9	76	US-08-851-362D-21	Sequence 21, App1
24	11	57.9	78	US-09-248-796A-15584	Sequence 15584, A
25	11	57.9	79	US-09-248-796A-23105	Sequence 23105, A
26	11	57.9	84	US-09-471-276-816	Sequence 816, App
27	11	57.9	86	US-09-252-991A-29383	Sequence 29383, A

ALIGNMENTS

28	11	57.9	88	2	US-09-905-243-34	Sequence 34, App1
29	11	57.9	91	2	US-10-330-613A-64	Sequence 64, App1
30	11	57.9	92	1	US-08-273-146-45	Sequence 45, App1
31	11	57.9	92	1	US-08-273-146-53	Sequence 53, App1
32	11	57.9	93	2	US-10-330-613A-44	Sequence 44, App1
33	11	57.9	95	2	US-09-472-087-94	Sequence 27, App1
34	11	57.9	95	2	US-09-627-896B-27	Sequence 54, App1
35	11	57.9	95	2	US-10-194-975-54	Sequence 54, App1
36	11	57.9	95	2	US-10-194-975-55	Sequence 55, App1
37	11	57.9	95	2	US-10-194-975-58	Sequence 58, App1
38	11	57.9	95	2	US-10-194-975-59	Sequence 59, App1
39	11	57.9	95	2	US-10-194-975-60	Sequence 60, App1
40	11	57.9	95	2	US-10-194-975-61	Sequence 61, App1
41	11	57.9	95	2	US-10-194-975-62	Sequence 62, App1
42	11	57.9	95	2	US-10-194-975-65	Sequence 65, App1
43	11	57.9	95	2	US-10-194-975-66	Sequence 66, App1
44	11	57.9	95	2	US-10-194-975-67	Sequence 67, App1
45	11	57.9	95	2	US-10-194-975-69	Sequence 69, App1

RESULT 1
US-08-540-412-123
Sequence 123, Application US/08540412
Patent No. 5866679
GENERAL INFORMATION:
APPLICANT: Defeo-Jones, Deborah
APPLICANT: Feng, Dong-Mei
APPLICANT: Garbky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oliffe, Allen I.
TITLE OF INVENTION: NOVEL PEPTIDES
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTIARD
STREET: 126 E. Lincoln Avenue, P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,412
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mutiard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 192531C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
TELEFAX: (908)594-3903
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-540-412-123
Query Match 57.9%; Score 11; DB 1; Length 11;
Best Local Similarity 33.3%; Pred No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0;

QY 4 YXXXXL 9
|
DB 6 YASSSL 11

RESULT 2

US-08-540-412-191
; Sequence 191, Application US/08540412
; Patent No. 5866679
; GENERAL INFORMATION:
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Feng, Dong-Mei
; APPLICANT: Garsky, Victor M.
; APPLICANT: Jones, Raymond E.
; APPLICANT: Oliffe, Allen I.
; TITLE OF INVENTION: NOVEL PEPTIDES
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID A. MUTHARD
; STREET: 126 E. Lincoln Avenue, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,412
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 192531C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-540-412-191

Query Match 57.9%; Score 11; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
|
DB 6 YASSSL 11

RESULT 3
US-09-051-342-123
; Sequence 123, Application US/09051342
; Patent No. 6130204
; GENERAL INFORMATION:
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Feng, Dong-Mei
; APPLICANT: Garsky, Victor M.
; APPLICANT: Jones, Raymond E.
; APPLICANT: Oliffe, Allen I.
; TITLE OF INVENTION: NOVEL PEPTIDES
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID A. MUTHARD

STREET: 126 E. Lincoln Avenue, P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,342
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 192531CY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-09-051-342-123

Query Match 57.9%; Score 11; DB 2; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
|
DB 6 YASSSL 11

RESULT 4
US-09-051-342-191
; Sequence 191, Application US/09051342
; Patent No. 6130204
; GENERAL INFORMATION:
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Feng, Dong-Mei
; APPLICANT: Garsky, Victor M.
; APPLICANT: Jones, Raymond E.
; APPLICANT: Oliffe, Allen I.
; TITLE OF INVENTION: NOVEL PEPTIDES
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID A. MUTHARD
; STREET: 126 E. Lincoln Avenue, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,342
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A.
; REGISTRATION NUMBER: 35,297

REFERENCE/DOCKET NUMBER: 192531CY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-051-342-191

Query Match 57.9%; Score 11; DB 2; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
|
Db 6 YASSSL 11

RESULT 5
US-08-468-161-123
Sequence 123, Application US/08468161
Patent No. 6143864
GENERAL INFORMATION:
APPLICANT: Defeo-Jones, Deborah
APPLICANT: Feng, Dong-Mei
APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oloff, Allen I.
TITLE OF INVENTION: NOVEL PEPTIDES
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD
STREET: 126 E. Lincoln Avenue, P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,161
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 192531B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-468-161-123

Query Match 57.9%; Score 11; DB 2; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
|
Db 6 YASSSL 11

RESULT 6
US-09-051-759-123
Sequence 123, Application US/09051759
Patent No. 6177404
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Defeo-Jones, Deborah
APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oloff, Allen I.
APPLICANT: Scolnick, Edward M.
TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
FILE REFERENCE: 19560P
CURRENT APPLICATION NUMBER: US/09/051,759
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: 60/005,664
PRIOR FILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 123
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
US-09-051-759-123

Query Match 57.9%; Score 11; DB 2; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
|
Db 6 YASSSL 11

RESULT 7
US-09-051-759-191
Sequence 191, Application US/09051759
Patent No. 6177404
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Defeo-Jones, Deborah
APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oloff, Allen I.
APPLICANT: Scolnick, Edward M.
TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
FILE REFERENCE: 19560P
CURRENT APPLICATION NUMBER: US/09/051,759
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: 60/005,664
PRIOR FILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 191
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
US-09-051-759-191

Query Match 57.9%; Score 11; DB 2; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
| |
Db 6 YASSSL 11

RESULT 8
PCT-US95-08156-123

; Sequence 123, Application PC/TUS9508156
; GENERAL INFORMATION:

; APPLICANT: Defeo-Jones, Deborah

; APPLICANT: Feng, Dong-Mei

; APPLICANT: Gareky, Victor M.

; APPLICANT: Jones, Raymond E.

; APPLICANT: Olf, Allen I.

; TITLE OF INVENTION: NOVEL PEPTIDES

; NUMBER OF SEQUENCES: 146

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID A. MUTHARD

; STREET: 126 E. Lincoln Avenue, P.O. BOX 2000

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: U.S.A.

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08156

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Muthard, David A.

; REGISTRATION NUMBER: 35,297

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908)594-3903

; TELEFAX: (908)594-4720

; INFORMATION FOR SEQ ID NO: 123:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; PCT-US95-08156-123

Query Match 57.9%; Score 11; DB 4; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
| |
Db 6 YASSSL 11

RESULT 9

; Patent No. 5219837

; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,

; WILLIAM V.

; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION

; OF CELLS

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/541,779

; FILING DATE: 21-JUN-1990

; SEQ ID NO:5

; LENGTH: 18

; 5219837-5

Query Match 57.9%; Score 11; DB 6; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
| |
Db 12 YSASTL 17

RESULT 10

; US-09-513-365A-5

; Sequence 5, Application US/09513365A

; Patent No. 6790948

; GENERAL INFORMATION:

; APPLICANT: Harris, Curtis C

; APPLICANT: Nagashima, Makoto

; APPLICANT: Government of United States as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: New Tumor Suppressor Gene P3JING2

; FILE REFERENCE: 015280-376100US

; CURRENT APPLICATION NUMBER: US/09/513,365A

; CURRENT FILING DATE: 2000-02-25

; PRIOR APPLICATION NUMBER: US 60/121,891

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: peptide 7-26

; US-09-513-365A-5

Query Match 57.9%; Score 11; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
| |
Db 4 YSSAAL 9

RESULT 11

; US-08-905-223-22

; Sequence 22, Application US/08905223

; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.

; APPLICANT: Lacroix, Bruno

; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: WIN95

; SOFTWARE: Word


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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/905,223
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Israelien, Ned A.
/ REGISTRATION NUMBER: 29,655
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 235-8550
/ TELEFAX: (619) 235-0176
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 37 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: LINEAR
/ MOLECULE TYPE: PROTEIN
/ ORIGINAL SOURCE:
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 1..37
/ IDENTIFICATION METHOD: Von Heijne matrix
/ OTHER INFORMATION: score 5.9
/ OTHER INFORMATION: seq LSVASSALSPLCT/AP
/ US-08-905-223-22

Query Match          57.9%; Score 11; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      4 YXXXXL 9
      |
Db      27 YASSAL 32

RESULT 12
US-09-247-155-22
/ Sequence 22, Application US/09247155A
/ Patent No. 6312922
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, Jean-Baptiste
/ APPLICANT: Duclert, Aymeric
/ APPLICANT: Bougueleret, Lydie
/ TITLE OF INVENTION: Complementary DNAs
/ FILE REFERENCE: GENSET.021A
/ CURRENT APPLICATION NUMBER: US/09/247,155A
/ CURRENT FILING DATE: 1999-02-09
/ EARLIER APPLICATION NUMBER: 60/074,121
/ EARLIER FILING DATE: 1998-02-09
/ EARLIER APPLICATION NUMBER: 60/081,563
/ EARLIER FILING DATE: 1998-04-13
/ EARLIER APPLICATION NUMBER: 60/096,116
/ EARLIER FILING DATE: 1998-08-10
/ EARLIER APPLICATION NUMBER: 60/099,273
/ EARLIER FILING DATE: 1998-10-04
/ NUMBER OF SEQ ID NOS: 182
/ SOFTWARE: Patent.pm
/ SEQ ID NO 22
/ LENGTH: 37
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: 1..37
/ OTHER INFORMATION: Von Heijne matrix
/ OTHER INFORMATION: score 5.9
/ OTHER INFORMATION: seq LSVASSALSPLCT/AP
/ US-09-247-155-22

Query Match          57.9%; Score 11; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      4 YXXXXL 9
      |
Db      27 YASSAL 32
```

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OY      4 YXXXXL 9
      |
Db      27 YASSAL 32

RESULT 13
US-09-663-600A-22
/ Sequence 22, Application US/09663600A
/ Patent No. 6573068
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, Jean-Baptiste
/ APPLICANT: Duclert, Aymeric
/ APPLICANT: Bougueleret, Lydie
/ TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
/ FILE REFERENCE: 31.US3.CIP
/ CURRENT APPLICATION NUMBER: US/09/663,600A
/ CURRENT FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: 09/191,997
/ PRIOR FILING DATE: 1998-11-13
/ PRIOR APPLICATION NUMBER: 60/066,677
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/069,957
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/074,121
/ PRIOR FILING DATE: 1998-02-09
/ PRIOR APPLICATION NUMBER: 60/081,563
/ PRIOR FILING DATE: 1998-04-13
/ PRIOR APPLICATION NUMBER: 60/096,116
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/099,273
/ PRIOR FILING DATE: 1998-09-04
/ NUMBER OF SEQ ID NOS: 229
/ SOFTWARE: Patent.pm
/ SEQ ID NO 22
/ LENGTH: 37
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: 1..37
/ OTHER INFORMATION: Von Heijne matrix
/ OTHER INFORMATION: score 5.9
/ OTHER INFORMATION: seq LSVASSALSPLCT/AP
/ US-09-663-600A-22

Query Match          57.9%; Score 11; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      4 YXXXXL 9
      |
Db      27 YASSAL 32

RESULT 14
US-09-903-190-22
/ Sequence 22, Application US/09903190
/ Patent No. 6936692
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, Jean-Baptiste
/ APPLICANT: Duclert, Aymeric
/ APPLICANT: Bougueleret, Lydie
/ TITLE OF INVENTION: Complementary DNAs
/ FILE REFERENCE: GENSET.021A
/ CURRENT APPLICATION NUMBER: US/09/903,190
/ CURRENT FILING DATE: 2001-07-11
/ PRIOR APPLICATION NUMBER: US/09/247,155A
/ PRIOR FILING DATE: 1999-02-09
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO: 22
LENGTH: 37
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..37
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LSYASSALSPLCT/AP
US-09-903-190-22

Query Match 57.9%; Score 11; DB 2; Length 37;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 27 YASSAL 32

RESULT 15
US-08-812-586-40
Sequence 40, Application US/08812586
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David Tilson
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-40

Query Match 57.9%; Score 11; DB 2; Length 40;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 15 YAASTL 20

Search completed: November 29, 2005, 23:04:23
Job time : 24.8636 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2005, 22:52:34 ; Search time 77.9545 Seconds
(without alignments)
53.599 Million cell updates/sec

Title: US-10-019-198a-5
Perfect score: 19
Sequence: 1 XXXXXXXXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	57.9	17	US-10-105-545-8	Sequence 8, Appli
2	11	57.9	17	US-10-120-835-65	Sequence 65, Appl
3	11	57.9	17	US-11-073-349-65	Sequence 21, Appl
4	11	57.9	18	US-10-105-545-21	Sequence 54, Appl
5	11	57.9	18	US-10-409-643-54	Sequence 66, Appl
6	11	57.9	19	US-10-120-835-66	Sequence 2, Appli
7	11	57.9	19	US-11-073-349-66	Sequence 6, Appli
8	11	57.9	20	US-10-197-945A-2	Sequence 609, App
9	11	57.9	20	US-10-176-013-616	Sequence 5, Appli
10	11	57.9	20	US-10-776-013-616	Sequence 616, App
11	11	57.9	20	US-10-868-270-5	Sequence 5, Appli
12	11	57.9	27	US-10-424-599-275349	Sequence 275349,
13	11	57.9	28	US-10-120-835-67	Sequence 67, Appl
14	11	57.9	28	US-11-073-349-67	Sequence 67, Appl
15	11	57.9	30	US-10-425-115-287301	Sequence 287301,
16	11	57.9	30	US-10-424-599-250421	Sequence 250421,
17	11	57.9	37	US-09-903-190-22	Sequence 22, Appl
18	11	57.9	37	US-10-319-763-22	Sequence 22, Appl
19	11	57.9	37	US-10-437-963-153132	Sequence 153132,
20	11	57.9	37	US-10-930-331-22	Sequence 22, Appl
21	11	57.9	38	US-10-437-963-120714	Sequence 120714,
22	11	57.9	40	US-10-425-115-361971	Sequence 361971,
23	11	57.9	41	US-10-276-774-2215	Sequence 2215, Ap
24	11	57.9	43	US-10-109-048-661	Sequence 661, App
25	11	57.9	44	US-10-767-701-61017	Sequence 61017, A
26	11	57.9	44	US-10-424-599-208666	Sequence 208666,
27	11	57.9	45	US-10-109-048-869	Sequence 869, App

ALIGNMENTS

28	11	57.9	45	4	US-10-425-115-354302	Sequence 354302,
29	11	57.9	48	4	US-10-424-599-169349	Sequence 169349,
30	11	57.9	49	4	US-10-437-963-142578	Sequence 142578,
31	11	57.9	49	4	US-10-425-115-201880	Sequence 201880,
32	11	57.9	49	4	US-10-425-115-321205	Sequence 321205,
33	11	57.9	49	4	US-10-425-115-325114	Sequence 325114,
34	11	57.9	50	3	US-09-978-360A-624	Sequence 624, App
35	11	57.9	50	3	US-10-425-115-321893	Sequence 321893,
36	11	57.9	50	6	US-11-075-234-379	Sequence 379, App
37	11	57.9	51	4	US-10-424-599-154170	Sequence 154170,
38	11	57.9	52	4	US-10-218-102-329	Sequence 329, App
39	11	57.9	52	4	US-10-425-115-366925	Sequence 366925,
40	11	57.9	53	4	US-10-424-599-217394	Sequence 217394,
41	11	57.9	54	5	US-10-866-499-933	Sequence 933, App
42	11	57.9	55	4	US-10-424-599-171812	Sequence 171812,
43	11	57.9	55	4	US-10-424-599-199688	Sequence 199688,
44	11	57.9	55	4	US-10-437-963-179375	Sequence 179375,
45	11	57.9	55	4	US-10-425-115-317178	Sequence 317178,

RESULT 1
US-10-105-545-8
Sequence 8, Application US/10105545
Publication No. US20030144479A1
GENERAL INFORMATION:
APPLICANT: Mark, Greene I.
APPLICANT: Williams, William V.
APPLICANT: Weiner, David B.
APPLICANT: Cohen, Jeffrey A.
APPLICANT: Kleber-Emmons, Thomas
APPLICANT: Williams, Robert M.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING
TITLE OF INVENTION: SAME
FILE REFERENCE: 4040/11492US2
CURRENT APPLICATION NUMBER: US/10/105,545
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 08/752,816
PRIOR FILING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: US 07/940,654
PRIOR FILING DATE: 1992-09-03
PRIOR APPLICATION NUMBER: US 07/702,833
PRIOR FILING DATE: 1991-05-20
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR FILING DATE: 1989-03-21
PRIOR APPLICATION NUMBER: US 07/074,264
PRIOR FILING DATE: 1987-07-16
PRIOR APPLICATION NUMBER: US 07/462,542
PRIOR FILING DATE: 1990-01-09
PRIOR APPLICATION NUMBER: US 07/648,303
PRIOR FILING DATE: 1991-01-25
PRIOR APPLICATION NUMBER: US 07/685,881
PRIOR FILING DATE: 1991-04-15
PRIOR APPLICATION NUMBER: US 07/574,391
PRIOR FILING DATE: 1990-08-27
PRIOR APPLICATION NUMBER: US 07/194,026
PRIOR FILING DATE: 1988-05-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-105-545-8
Query Match 57.9%; Score 11; DB 4; Length 17;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 11 YSASTL 16

RESULT 2

US-10-120-835-65
; Sequence 65, Application US/10120835
; Publication No. US20040018189A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve C.
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Saffran, Douglas
; APPLICANT: Morrison, Robert J. M.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20061.00
; CURRENT APPLICATION NUMBER: US/10/120,835
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/286,630
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/300,373
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-120-835-65

Query Match 57.9%; Score 11; DB 4; Length 17;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 5 YSTTTL 10

RESULT 3

US-11-073-349-65
; Sequence 65, Application US/11073349
; Publication No. US2005021211A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve C.
; APPLICANT: Afari, Daniel E. H.
; APPLICANT: Saffran, Douglas
; APPLICANT: Morrison, Robert J. M.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20061.00
; CURRENT APPLICATION NUMBER: US/11/073,349
; CURRENT FILING DATE: 2005-03-03

; PRIOR APPLICATION NUMBER: US/10/120,835
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/286,630
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/300,373
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-073-349-65

Query Match 57.9%; Score 11; DB 6; Length 17;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 5 YSTTTL 10

RESULT 4

US-10-105-545-21
; Sequence 21, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffery A.
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING
; FILE REFERENCE: 4040/11492US2
; CURRENT APPLICATION NUMBER: US/10/105,545
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-105-545-21

Query Match 57.9%; Score 11; DB 4; Length 18;

Best Local Similarity 33.3%; Pred. No. 4e+03; Indels 4; Gaps 0;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4 YXXXXL 9
DB 12 YSASTL 17

RESULT 5

US-10-409-643-54
Sequence 54, Application US/10409643
Publication No. US20030235577A1
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven
APPLICANT: Hartzell, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREVENTING AND TREATING MICROBIAL IN
FILE REFERENCE: B00801.70281 US
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,649
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
LENGTH: 18
TYPE: PRT
ORGANISM: Mus musculus
US-10-409-643-54

Query Match 57.9%; Score 11; DB 4; Length 18;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 9 YSASTL 14

RESULT 6

US-10-120-835-66
Sequence 66, Application US/10120835
Publication No. US20040018189A1
GENERAL INFORMATION:
APPLICANT: Ageneys, Inc.
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raito, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Mitchell, Steve C.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Saffran, Douglas
APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 19
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-120-835-66

Query Match 57.9%; Score 11; DB 4; Length 19;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match 57.9%; Score 11; DB 4; Length 19;
Best Local Similarity 33.3%; Pred. No. 4.1e+03; Indels 4; Gaps 0;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 6 YSTTTL 11

RESULT 7

US-11-073-349-66
Sequence 66, Application US/11073349
Publication No. US20050214211A1
GENERAL INFORMATION:
APPLICANT: Ageneys, Inc.
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raito, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Mitchell, Steve C.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Saffran, Douglas
APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILING DATE: 2005-03-03
PRIOR APPLICATION NUMBER: US/10/120,835
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 19
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-073-349-66

Query Match 57.9%; Score 11; DB 6; Length 19;
Best Local Similarity 33.3%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 YXXXXL 9
DB 6 YSTTTL 11

RESULT 8

US-10-197-945A-2
Sequence 2, Application US/10197945A
Publication No. US20040014148A1
GENERAL INFORMATION:
APPLICANT: Masuda, Seishan
APPLICANT: Kinoshita, Todd M.
APPLICANT: Warner, Justin B.
APPLICANT: Kinoshita, Taisei
APPLICANT: Bennett, Mark K.
APPLICANT: Anderson, David C.
TITLE OF INVENTION: Methods of Identifying Compounds that Modulate IL-4 Receptor-Med
FILE REFERENCE: RIGL-013/00US
CURRENT APPLICATION NUMBER: US/10/197,945A
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide generated by a combinatorial library
US-10-197-945A-2

Query Match 57.9%; Score 11; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 2 YTSNAL 7

RESULT 9
US-10-776-013-609
Sequence 609, Application US/10776013
Publication No. US2004026056A1
GENERAL INFORMATION:
APPLICANT: MYRIAD GENETICS, INC.
APPLICANT: Roch, Jean-Marc
APPLICANT: Bartel, Paul
APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
FILE REFERENCE: 1600.24
CURRENT APPLICATION NUMBER: US/10/776,013
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113534
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/141243
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/975072
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 10/194967
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
SOFTWARE: PatentIn version 3.2
SEQ ID NO 609
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-776-013-609

Query Match 57.9%; Score 11; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 9 YATATL 14

RESULT 10
US-10-776-013-616
Sequence 616, Application US/10776013
Publication No. US2004026056A1
GENERAL INFORMATION:

APPLICANT: MYRIAD GENETICS, INC.
APPLICANT: Roch, Jean-Marc
APPLICANT: Bartel, Paul
APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
FILE REFERENCE: 1600.24
CURRENT APPLICATION NUMBER: US/10/776,013
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113534
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/141243
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/975072
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 10/194967
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
SOFTWARE: PatentIn version 3.2
SEQ ID NO 616
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-776-013-616

Query Match 57.9%; Score 11; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 15 YATATL 20

RESULT 11
US-10-868-270-5
Sequence 5, Application US/10868270
Publication No. US2004023511A1
GENERAL INFORMATION:
APPLICANT: Nagashima, Makoto
APPLICANT: Government of United States as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
FILE REFERENCE: 015280-376100US
CURRENT APPLICATION NUMBER: US/10/868,270
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/121,891
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide 7-26
US-10-868-270-5

Query Match 57.9%; Score 11; DB 5; Length 20;

Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 4 YSSNAL 9

RESULT 12

US-10-424-599-275349
Sequence 275349, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Title of Invention: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285884

SEQ ID NO 275349

LENGTH: 27

TYPE: PRT

ORGANISM: Glycine max

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_90660C.1.pep

US-10-424-599-275349

Query Match Best Local Similarity 57.9%; Score 11; DB 4; Length 27;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 12 YTSSTL 17

US-10-120-835-67
Sequence 67, Application US/10120835

Publication No. US20040018189A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Farris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Afari, Daniel E. H.

APPLICANT: Saffran, Douglas

APPLICANT: Morrison, Karen J. M.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Mangmao

APPLICANT: Jakobovitz, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
Title of Invention: ENTITLED 121P2A3 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20061.00

CURRENT APPLICATION NUMBER: US/10/120,835

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/300,373

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 67

LENGTH: 28

TYPE: PRT

ORGANISM: Homo Sapiens
US-10-120-835-67

Query Match Best Local Similarity 57.9%; Score 11; DB 4; Length 28;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 11 YSTTTL 16

US-11-073-349-67
Sequence 67, Application US/11073349

Publication No. US20050214211A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Farris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Afari, Daniel E. H.

APPLICANT: Saffran, Douglas

APPLICANT: Morrison, Karen J. M.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Mangmao

APPLICANT: Jakobovitz, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
Title of Invention: ENTITLED 121P2A3 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20061.00

CURRENT APPLICATION NUMBER: US/11/073,349

CURRENT FILING DATE: 2005-03-03

PRIOR APPLICATION NUMBER: US/10/120,835

PRIOR FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/282,739

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60/286,630

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/300,373

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 67

LENGTH: 28

TYPE: PRT

ORGANISM: Homo Sapiens

US-11-073-349-67

Query Match Best Local Similarity 57.9%; Score 11; DB 6; Length 28;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 11 YSTTTL 16

US-10-425-115-287301
Sequence 287301, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

Title of Invention: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 287301
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_25114C.1.pcp
US-10-425-115-287301
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Query Match          57.9% Score 11; DB 4; Length 30;
Best Local Similarity 33.3%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      4 YXXXXL 9
         |  |
Db       4 YAAATL 9
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Search completed: November 29, 2005, 23:10:29
Job time : 78.9545 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2005, 22:45:19 ; Search time 2.5 Seconds
(without alignments)
12.124 Million cell updates/sec

Title: US-10-019-198a-5
Perfect score: 19
Sequence: 1 XXXXXXXXX 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdp.*
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4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdp.*
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6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdp.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdp.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	57.9	83	1	US-10-510-386-114
2	11	57.9	96	7	US-11-144-248-40
3	11	57.9	96	7	US-11-144-248-42
4	11	57.9	107	1	US-10-507-662-41
5	11	57.9	107	1	US-10-507-662-41
6	11	57.9	108	1	US-10-986-501-151
7	11	57.9	236	7	US-11-144-248-48
8	11	57.9	236	7	US-11-144-248-52
9	11	57.9	241	7	US-11-054-515-1577
10	11	57.9	241	7	US-11-054-515-1932
11	11	57.9	241	7	US-11-054-515-2054
12	11	57.9	242	7	US-11-054-515-1915
13	11	57.9	244	7	US-11-054-515-82
14	11	57.9	244	7	US-11-054-515-164
15	11	57.9	244	7	US-11-054-515-261
16	11	57.9	244	7	US-11-054-515-280
17	11	57.9	244	7	US-11-054-515-1881
18	11	57.9	246	7	US-11-054-515-2075
19	11	57.9	247	7	US-11-054-515-3240
20	11	57.9	248	7	US-11-054-515-1446
21	11	57.9	249	7	US-11-054-515-1635
22	11	57.9	250	7	US-11-054-515-1174
23	11	57.9	251	7	US-11-054-515-1310
24	11	57.9	251	7	US-11-054-515-1921
25	11	57.9	253	7	US-11-054-515-936

26	11	57.9	316	1	US-10-510-386-244	Sequence 244, App
27	11	57.9	353	7	US-11-137-465-44	Sequence 44, Appl
28	11	57.9	448	7	US-11-137-465-45	Sequence 45, Appl
29	11	57.9	708	1	US-10-821-234-917	Sequence 917, App
30	11	57.9	775	1	US-10-131-826A-120	Sequence 120, App
31	10	52.6	18	1	US-10-997-697-5	Sequence 5, Appl1
32	10	52.6	23	1	US-10-997-697-4	Sequence 4, Appl1
33	10	52.6	24	1	US-10-997-697-3	Sequence 3, Appl1
34	10	52.6	29	1	US-10-997-697-2	Sequence 2, Appl1
35	10	52.6	29	1	US-10-997-697-7	Sequence 8, Appl1
36	10	52.6	29	1	US-10-997-697-8	Sequence 11, Appl1
37	10	52.6	29	1	US-10-997-697-11	Sequence 12, Appl1
38	10	52.6	29	1	US-10-997-697-12	Sequence 13, Appl1
39	10	52.6	29	1	US-10-997-697-13	Sequence 14, Appl1
40	10	52.6	29	1	US-10-997-697-14	Sequence 9, Appl1
41	10	52.6	62	1	US-10-493-864A-9	Sequence 10, Appl1
42	10	52.6	100	7	US-11-144-248-10	Sequence 1708, Ap
43	10	52.6	103	1	US-10-793-626-1708	Sequence 2074, Ap
44	10	52.6	103	1	US-10-793-626-2074	Sequence 6, Appl1
45	10	52.6	107	7	US-11-077-978-6	

ALIGNMENTS

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RESULT 1
US-10-510-386-114
; Sequence 114, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjørke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-114

Query Match      57.9%  Score 11; DB 1; Length 83;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0;
Gaps 0;

QY      4 YXXXXL 9
DB      23 YSAAAL 28

RESULT 2
US-11-144-248-40
; Sequence 40, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
```

;; PRIOR APPLICATION NUMBER: 60/259,927
;; PRIOR FILING DATE: 2001-01-05
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 40
;; LENGTH: 96
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-248-40

Query Match 57.9%; Score 11; DB 7; Length 96;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 49 YAASSL 54

RESULT 3

US-11-144-248-42
;; Sequence 42, Application US/11144248
;; Publication No. US20050244408A1
;; GENERAL INFORMATION:
;; APPLICANT: Beebe, Bruce D.
;; APPLICANT: Miller, Penelope E.
;; APPLICANT: Moyer, James D.
;; APPLICANT: Corvalan, Jose R.
;; APPLICANT: Gallo, Michael
;; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
;; FILE REFERENCE: ABX-PR2
;; CURRENT APPLICATION NUMBER: US/11/144,248
;; CURRENT FILING DATE: 2005-06-02
;; PRIOR APPLICATION NUMBER: US/10/039,591
;; PRIOR FILING DATE: 2002-01-04
;; PRIOR APPLICATION NUMBER: 60/259,927
;; PRIOR FILING DATE: 2001-01-05
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 42
;; LENGTH: 96
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-248-42

Query Match 57.9%; Score 11; DB 7; Length 96;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 49 YAASSL 54

RESULT 4

US-10-507-662-40
;; Sequence 40, Application US/10507662
;; Publication No. US20050255102A1
;; GENERAL INFORMATION:
;; APPLICANT: BIOGEN, INC.
;; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
;; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
;; FILE REFERENCE: A136PCT
;; CURRENT APPLICATION NUMBER: US/10/507,662
;; CURRENT FILING DATE: 2004-09-13
;; PRIOR APPLICATION NUMBER: 60/364,991
;; PRIOR FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: 60/426,286
;; PRIOR FILING DATE: 2002-11-13
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 40

;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-507-662-40

Query Match 57.9%; Score 11; DB 1; Length 107;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 49 YAASSL 54

RESULT 5

US-10-507-662-41
;; Sequence 41, Application US/10507662
;; Publication No. US20050255102A1
;; GENERAL INFORMATION:
;; APPLICANT: BIOGEN, INC.
;; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
;; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
;; FILE REFERENCE: A136PCT
;; CURRENT APPLICATION NUMBER: US/10/507,662
;; CURRENT FILING DATE: 2004-09-13
;; PRIOR APPLICATION NUMBER: 60/364,991
;; PRIOR FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: 60/426,286
;; PRIOR FILING DATE: 2002-11-13
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 41
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-507-662-41

Query Match 57.9%; Score 11; DB 1; Length 107;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YXXXXL 9
DB 49 YAASSL 54

RESULT 6

US-10-986-501-151
;; Sequence 151, Application US/10986501
;; Publication No. US20050244845A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruden et al.
;; TITLE OF INVENTION: 90 Human Secreted Proteins
;; FILE REFERENCE: P2013P2C1
;; CURRENT APPLICATION NUMBER: US/10/986,501
;; CURRENT FILING DATE: 2004-11-12
;; PRIOR APPLICATION NUMBER: US/10/621,363
;; PRIOR FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: 09/969,730
;; PRIOR FILING DATE: 2001-10-06
;; PRIOR APPLICATION NUMBER: 09/774,639
;; PRIOR FILING DATE: 2001-02-01
;; PRIOR APPLICATION NUMBER: 60/238,291
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 09/244,112
;; PRIOR FILING DATE: 1999-02-04
;; PRIOR APPLICATION NUMBER: PCT/US98/16235
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/056,371
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 60/056,732
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 60/056,366

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/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 151
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-151
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Query Match          57.9%; Score 11; DB 1; Length 108;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 4 YXXXXL 9
DB 79 YSSAAL 84
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RESULT 7
US-11-144-248-48
/ Sequence 48, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 48
/ LENGTH: 236
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-48
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Query Match          57.9%; Score 11; DB 7; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
QY 4 YXXXXL 9
DB 71 YAASL 76
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RESULT 8
US-11-144-248-52
/ Sequence 52, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
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/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 236
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-52
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Query Match          57.9%; Score 11; DB 7; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 4 YXXXXL 9
DB 71 YAASL 76
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RESULT 9
US-11-054-515-1577
/ Sequence 1577, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/240,816
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1577
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1577
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Query Match          57.9%; Score 11; DB 7; Length 241;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 4 YXXXXL 9
DB 182 YAASL 187
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RESULT 10
US-11-054-515-1932
/ Sequence 1932, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
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```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1932
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1932
```

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Query Match      57.9%; Score 11; DB 7; Length 241;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      4 YXXXXL 9
Db      182 YAASTL 187
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RESULT 11
US-11-054-515-2054
; Sequence 2054, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
```

```
; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2054
```

```
Query Match      57.9%; Score 11; DB 7; Length 241;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      4 YXXXXL 9
Db      182 YAASTL 187
```

```
RESULT 12
US-11-054-515-1915
; Sequence 1915, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1915
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1915

Query Match      57.9%; Score 11; DB 7; Length 242;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      4 YXXXXL 9
Db      183 YAASTL 188
```

```
RESULT 13
US-11-054-515-82
; Sequence 82, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
```

```

; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 82
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-82

```

```

Query Match      57.9%; Score 11; DB 7; Length 244;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 YXXXXL 9
DB      185 YAASTL 190

```

```

RESULT 14
US-11-054-515-164
; Sequence 164, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 164
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-164

```

```

Query Match      57.9%; Score 11; DB 7; Length 244;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 YXXXXL 9
DB      185 YAASTL 190

```

```

RESULT 15
US-11-054-515-261
; Sequence 261, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 261
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-261

```

```

Query Match      57.9%; Score 11; DB 7; Length 244;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      4 YXXXXL 9
DB      185 YAASTL 190

```

Search completed: November 29, 2005, 23:04:39
Job time : 3.75 secs

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